



Eighth
ALL INDIA
CONFERENCE
ON
CYTOLOGY
AND
GENETICS

JANUARY 23-25-2001



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EIGHTH **ALL INDIA CONFERENCE ON CYTOLOGY AND GENETICS**

January 23-25, 2001



Bangalore University

&

Society of Cytologists and Geneticists



Souvenir & Abstracts

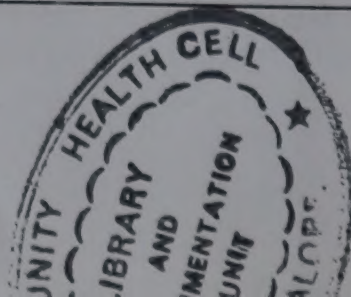
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PREFACE

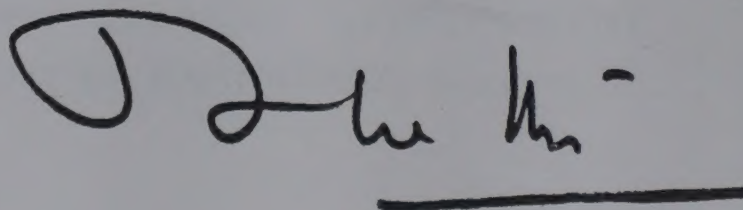
The Indian Society of Cytologists and Geneticists is organizing its Eighth Annual Convention at the Centre for Applied Genetics of Bangalore University. The said Conference is being sponsored by Bangalore University and the Indian Society of Cytologists and Geneticists. On behalf of the National Executive and Local Organizing Committees, I take this opportunity to extend a warm welcome to all the delegates and invited guests to attend the Eighth All India Conference on Cytology and Genetics at the Senate Hall, Central College Campus, Bangalore University, Bangalore 560 001 from January 23rd-25th, 2001.

Bangalore, the Capital City of the State of Karnataka is known both as the 'Science City' as well as the 'Silicon Valley' of India with a rich cultural heritage and massive industrial growth. It is one of the fastest growing cities of the South East Asia.

The Congress is being attended by over 300 delegates from all over the country. The scientific programmes have been arranged so as to allow maximum time for deliberations and discussions and evaluate progress in scientific research.

We look forward to a successful conference, which will go a long way in understanding the recent advances in cytogenetics and allied subjects.

I once again welcome you all to Bangalore and to the conference and look forward to your active participation in the deliberations of the Eighth All India Conference on Cytology and Genetics.



(N.J. SHETTY)

Chairman and Organizing Secretary
Eighth All India Conference on
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EIGHTH **ALL INDIA CONFERENCE ON CYTOLOGY AND GENETICS**

January 23-25, 2001

Programme

Tuesday - January 23, 2001

08.00 Hrs.	Registration
09.30 Hrs.	Inauguration
11.00 Hrs.	TEA
11.30 Hrs.	Keynote Address
12.00 Hrs.	Presidential Address / Special Lecture
12.30 Hrs.	LUNCH
14.00 Hrs.	Scientific Session - I
16.00 Hrs.	TEA
16.15 Hrs.	Scientific Session - II
18.00 Hrs.	At Home (Cultural Programme)/EC Meeting of SCGI
19.45 Hrs.	DINNER

Wednesday - January 24, 2001

09.00 Hrs.	Scientific Session - III
10.45 Hrs.	TEA
11.00 Hrs.	Scientific Session -IV
13.00 Hrs.	LUNCH
14-00 Hrs.	Poster Session - I (Rajaji Hall)
15.00 Hrs.	TEA
15.15 Hrs.	Scientific Session - V / Session for Young Scientist Award
19.30 Hrs.	DINNER

Thursday, January 25, 2001

09.00 Hrs.	Scientific Session - VI
10.45 Hrs.	TEA
11.00 Hrs.	Scientific Session - VII
13.00 Hrs.	LUNCH
14.00 Hrs.	Poster Session - II (Rajaji Hall)
15.00 Hrs.	Valedictory Function / Concluding Session/General Body Meeting of SCGI (C1)
17.00 Hrs.	High TEA

PLENARY / INVITED LECTURES
(1 to 16 & 174)

CONTRIBUTED PAPERS
ORAL / POSTERS
(17 to 163 & 175)

CONTRIBUTED PAPERS
ORAL AWARD
(164 to 173)

1

FUNCTIONAL GENOMICS

G. PADMANABAN

Department of Biochemistry, Indian Institute of Science, Bangalore 560 012, Karnataka

The announcement of the completion of the human genome sequence has created a lot of excitement. Although the sequence is not fully complete and needs to be annotated, it has raised visions of unprecedented opportunities to discover new drugs, vaccines and diagnostics. The total number of genes in the human genome is still a matter of debate. It appears that the number of known genes in the human genome may not exceed 20-30%. Comparative genomics can help to identify more genes in the sequence. The greatest challenge will be to know the function of all the genes through a knowledge of the function of the proteins coded for. Many genes would just be coding for Open Reading Frames (ORF) of unknown function. Therefore, the identification of such proteins would involve isolating these proteins coded for by the ORFs and characterizing each through biochemical and structural approaches.

While , these studies are in progress, the utility of functional genomics has already become evident. DNA micro arrays are custom made and are being used to study the levels of expression of messenger RNA s between any two living cellular states. These arrays carry 5000 to 20, 000 probes and thus the expression patterns based on the hybridization of appropriately tagged mRNAs (c DNAs) to the probes that can be detected on the basis of fluorescent labeled ligands to bind to the tags are being analysed using the computer. These finger prints have already indicated a dramatic difference between normal cells and different types of cancer cells. Differences in host gene expression pattern is discernible between dormant and 'disease progression' states in specific infectious diseases. DNA micro arrays are becoming useful in Toxicogenomics and Pharmacogenomics. With the identification of newer genes in the human genome, one can hope that the molecular basis of more and more genetic disorders would be unraveled. This would pave the way for diagnosis and candidates for gene therapy. The availability of the genome sequences of pathogenic microorganisms has already led to the identification of unique genes with potential to be new drug targets or vaccine candidates.

A crucial issue is the identification and characterization of the protein pattern in the different situations discussed earlier. While , DNA microarrays can give the mRNA finger print, protein analysis would involve 2-D analysis and characterization of each protein spot. Post translational modifications such as phosphorylation of each protein spot. Post translational modifications such as phosphorylation and proteolytic processing would result in the number of protein species far exceeding the number of mRNAs and the subjects of proteomics and structural genomics are vital to carry out the objectives of functional genomics. All these would be great challenges in the 21st century, but there is great hope that all this knowledge would be useful in lessening the burden of human suffering.

2

BIOTECHNOLOGY IN SERICULTURE

K. P. GOPINATHAN

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Sericulture, the rearing of silkworms for the commercial production of silk has been practiced in India for more than two thousand years. Today six million people make a livelihood through sericulture, in the country. The productivity of silk in India works out to less than 2.5 to 3 Kg per annum amounting to a measly income of less than Rs. 3,000/- Evidently improvements in productivity both in terms of quality and quatity of silk are warranted to enhance the income and living standards of the silk farmer. Although significant advances have been made in the practice of sericulture over the years, primarily through genetic cross breeding and selection of improved races in terms of increased yield as well as disease resistance, these approaches have reached their limits. One certain way to advance further appears to be through biotechnology. Genetic manipulation of the silkworm races through transgenesis is a distinct possibility but this methodology is still at its infancy. Molecular breeding techniques by making use of the mapped microsatellite molecular markers offers another possibility to generate better races of silkworm.

An alternate method to improve the income for the silk farmer is to utilise the silkworms for production of materials other than silk. In this approach, exploitation of the high protein synthesizing capacity of the silkworm and the easy rearing methodologies taken together with the principles of baculovirus -based high level expression of cloned foreign

genes in insect cells are envisaged. The baculovirus-based high level expression of cloned foreign genes in insect cells are envisaged. The baculovirus Bm NPV, nuclear polyhedrosis virus normally pathogenic to the silkworms, can be genetically manipulated to harbour foreign genes of choice (eg: genes encoding proteins of biomedical importance) and used to infect the silkworm larvae. Such recombinant virus-infected larvae produce significant quantities of the foreign protein (encoded by the gene), that is biologically active. This possibility has been demonstrated and established by our own research team and provides potential for commercial application.

3

DNA TOPOISOMERASES FROM MYCOBACTERIA -AS MOLECULAR TARGETS FOR NEW DRUG DISCOVERY

V. NAGARAJA

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DNA topoisomerases are ubiquitous enzymes carrying out vital topological reactions during the process of replication, transcription and other DNA transaction processes. Since their function is essential for cell survival, the enzymes appear to be invaluable drug targets.

I shall describe topoisomerase functions and their importance. Our research efforts on different topoisomerases from mycobacteria -cloning, over-expression, biochemical characterization, etc will be presented. Finally, how this information is useful in developing new therapeutics against dreaded mycobacterial infections would be discussed.

4

BIOTECHNOLOGICAL TOOLS FOR THE CONTROL OF MALARIA VECTORS

N. J. SHETTY

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The challenge posed by insecticide resistance in mosquitoes has resulted in greater interest in mosquito genetics which has become one of the most rapidly growing areas of medical entomology. Resistance, with its

genetic basis has underlined the need for intensive genetic and cytogenetic research, especially on malaria vectors.

The replacement of wild mosquito populations with genetically defined lines of vector mosquitoes, refractory to the development of the malarial parasite is one possible method for controlling malaria. The refractory mosquito population would be incapable of transmitting the infection. In addition to this, there are certain chromosomal aberrations especially translocations and pericentric inversions associated with high levels of sterility and are potentially useful for genetic control measures. In order to achieve the genetic manipulation involving sterile males, releases can be enhanced by developing a method by which males can be easily separated from the females during mass production. Therefore, genetic sexing system for preferential elimination of females during early developmental stages is mandatory. The relevance of vector genetics and the role of genetics in vector control will be presented and the future prospects will also be discussed.

5

HUMAN GENETICS- PERSPECTIVES

I. M. THOMAS

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Man, probably realized many years ago, that there was a resemblance between parents and children and that certain characteristic features were being handed down from the parents to their progeny. Human genetics could thus be very easily defined as the study of inheritance and consequently, the study of genes.

The last 50 years has shown a veritable explosion in human genetics because of the discovery of DNA as the blueprint, by Watson and Crick. This has been followed recently by the introduction of gene therapy, which can be termed as the ultimate in therapy. Added to this was the completion of the genome sequencing in June 2000. However, this is only the beginning of functional genomics.

There are various areas in Human Genetics : Basic research : Clinical Genetics : Cytogenetics : Biochemical Genetics : Antenatal Genetics : Molecular Genetics and Genetic Counseling. According to McCusick there are over 11,000 genetic diseases. The diseases are Mendelian : Chromosomal : Multifactorial; somatic cell [eg : cancer] ; and Mitochondrial. The

question is now whether an adequate number of scientists are available to diagnose, investigate, treat, counsel and do basic research on genetic diseases? With a population of over one billion in India [estimates put mental retardation at 3% of any population] there would be a mentally retarded population of about 30 million, which in terms of comparison would be more than that of the population of Australia.

It is, therefore, important that, we Indians, realize that we need to put in more effort to look after our own countrymen with genetic diseases. It is needless to say that while these genetically altered people need help, both manpower and facilities are poor. The Indian Council of Medical Research has recently published a much-needed booklet on "Ethical Guidelines for Biomedical Research on Human Subjects." This, indeed, lays down guidelines to all biomedical scientists who should become aware of it.

6

HALF A CENTURY OF VECTOR GENETICS : THE PROGRESS, THE PROSPECTS AND THE PARADOX

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Mosquito transmitted human diseases such as malaria, filariasis, yellow fever, dengue and dengue hemorrhagic fevers and several viral encephalitides continue to pose some of the most serious public health problems in the world. Malaria alone causes clinical illness, often severe, in 300-500 million people and between 1.4 -2.6 million deaths each year. The epidemiology and distribution of many of these diseases has dramatically increased in recent years due to a variety of reasons. Consequently, many of these diseases have become virtually intractable. Global warming, if real, will further exacerbate the problem.

Although the discovery of the role of mosquitoes to transmit the malarial parasite to humans just about coincided with the "rediscovery" of Mendelism in Europe in 1900, vector genetics as a formal discipline dates back to mid 50's. Over the last half a century, much progress has been made in studying various aspects of genetics of mosquitoes, particularly involving several species of three principal genera, *Aedes*, *Culex* and *Anopheles*. Selected areas of this research involving isolation, and genetic map-

ping of morphological, biochemical, and molecular genetic markers, population genetics, and genome structure, organization and evolution will be briefly discussed. Information and insights gained from in-depth analyses of these areas, particularly transmission genetics, cytogenetics, genetics of chromosomal rearrangements and of mutagen -induced sexual sterility, have proved invaluable for the development of the theory and evaluation of the feasibility of genetic control of natural populations of vectors. As a result, mosquitoes represent some of the best studied organisms at various levels of genetic organization span, present a genetic paradox whereby the populations tend to rapidly evolve resistance to any introduced mechanism.

Recent research involving molecular genetic techniques to construct saturated, genetic and physical maps, isolation and cloning of refractory genes for vector incompetence, and vector transformation with molecular constructs of such genes with suitable and functional transporting systems, offer theoretically sound possibilities for extension of the concepts derived from classical genetic studies to control and/or manage vector transmitted diseases. Field releases of an appropriate molecular genetic mechanism in the not too-distant future, are contemplated , under sponsorship of multinational initiative. Such field releases, in the first instance, are likely to involve malaria at a suitable location in the continent of Africa.

7

BIOLOGICAL WARFARE AND BIOTERRORISM : A REAL THREAT

LT. GEN. D. RAGHUNATH (RETD.)

Sir Dorabji Tata Centre for Research in Tropical Diseases, Innovation Centre, Indian Institute of Science Campus, Bangalore 560 012, Karnataka

History is replete with accounts of pestilences that decimated human populations. Massive outbreaks of plague, cholera, smallpox, influenza, etc. have played major roles in human events. While these catastrophes were generally ascribed to 'evil spirits', wrath of Gods or deserved retribution for evil ways, shrewd observers (even in the Pre Christian era) realised that they were due to infectious agents. The effectiveness of the outbreaks of contagious diseases in causing social paralysis tempted ambitious conquerors to use them as military weapons. Probably , the only reason we have no record of such in ancient history is because the ability to strike at the enemy *alone* was not developed. Nevertheless, there are historical accounts of using diverse noxious biological substances as weapons including such materials as 'faeces, dead horses and fleas'. It has always been difficult to verify such

attacks. There is evidence that the attempts were not confined to military action, 'disgruntled' civilians and even some physicians resorted to this modality.

The rapid strides in the study of infectious diseases after the germ theory of infection was established, culminating in modern Molecular Biology, has been a major scientific achievement of the 20th Century. We have learnt how to handle infectious agents for the benefit for humanity. However, there is a flip side to this achievement, we have also acquired the ability to use them as destructive weapons. Biological weapons are now a days designed to infect human being, animals of economic importance, crops and the environment. In fact, biological weapons have been clubbed together with nuclear and chemical weapons as agents of man destruction.

Biological weapons are easy to produce, handle and disperse. They afford the attacker adequate time to escape and cause extensive damage. In fact, they are probably the most cost-effective agents of mass destruction. They are capable of being handled in small innocuous looking facilities. Thus, the individual or small group based Bioterrorism is a real danger.

Protection against Biological Warfare and Bioterrorism is based on awareness, medical and public health response, research and organisation. It is an International issue that is being addressed. However, there are regional overtones that require attention.

8

MOLECULAR GENETICS OF GENES REGULATING INFLORESCENCE DEVELOPMENT IN RICE

USHA VIJAYRAGHAVAN

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Some of the questions central of developmental biology are : How do cells arising from divisions of the fertilized egg become different from each other? How are these cells programmed to generate complex organs with many differentiated cell types? In the recent past there has been a rapid expansion of our understanding of how genes control these developmental process in model experimental systems, especially those from animal systems. Modern-day flowering plants : angiosperms, represent a diverse group of advanced plants, many species of which bear products of economic importance. In this large plant group the development of flowers,

is a highly regulated process. Understanding when, where and how flowers are formed will elucidate mechanisms that specify cell-fate in plants. Molecular genetics of floral homeotic genes in *Arabidopsis thaliana*, a model laboratory system, are revealing how 'master genes' dictate flowering and the stereotypic patterning of floral organs. A majority of these regulatory genes encode DNA-binding transcription factors, that dictate the activity of downstream target genes to control cell-fate. These *Arabidopsis* genes provide start points to study how related genes function in distantly related plant species.

My laboratory has been investigating the rice genes that control the formation and pattern of the rice inflorescence, flowers and floral organs therein. We study how the activity of regulatory proteins : i.e., transcription factors and signalling molecules, can alter a cell's fate and its proliferation. We have cloned and characterized some rice genes that are significantly similar in sequence to *Arabidopsis* genes that determine floral development. We have determined that the rice genes *OSL (RFL)*, *OsMADS1*, *OsMADS2* are transcribed in temporally and spatially regulated manner, specifically during rice inflorescence development. The rice *OSL* gene, a sequence homologue of the *Arabidopsis* floral identity gene : *LEAFY*, encodes a putative nuclear localized protein, with proline rich and acidic motifs that are typical of eukaryotic transcription factors. We find that *OSL* is expressed only at specific stages during development of the inflorescence. We suggest a function in determining the branched rice inflorescence and also in establishing the rice flower meristems. These data imply both evolutionarily conserved as well as species-specific functions for the rice *OSL* gene. Current studies include analysis of the expression pattern of *OSL* in rice strains with mutations that cause phenotypic changes in panicle development. We are also studying two other rice transcription factors : *OsMADS1* and *OsMADS2* that bear the DNA-binding MADS-box, found in other eukaryotic transcription factors. These genes are expressed only in flower primordia and further only in specific floral organ primordia. Through studying the consequences of mis-expression of *OsMADS1* in transgenic rice plants we infer that *OsMADS1* is required for the specification of the lemma and palea, grass floral organs analogous to sepals of dicot flowers. Thus these studies contribute to our understanding of how regulatory proteins in plants control the precise and invariant patterns in the flowering stem and flowers.

DNA VACCINES

P N RANGARAJAN

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A novel approach to the development of needed vaccines uses DNA for immunization. DNA represents the genetic blueprint for life. When DNA is used for immunization, the DNA in plasmid form provides the code for the vaccinating protein. The actual production of the immunizing protein takes place in the DNA-inoculated host, initiating both humoral and cellular immunity. DNA vaccines are administered in saline using hypodermic needles or by propelling DNA-coated gold beads into skin using gene guns. Recent results obtained in animal models indicate that this new technology may revolutionize the vaccination of humans. Protective immunity has been achieved for such major killers as diarrhea-causing viruses, tuberculosis-inducing bacteria, and malaria-inducing parasites. These new DNA vaccines also hold promise for being safer, less expensive, and easier to product and administer than conventional vaccines.

10

GENETICALLY MODIFIED PLANTS – PROSPECTS AND PROBLEMS

G.M. REDDY

INSA Sr. Scientist, Centre for Plant Molecular Biology, Osmania University, Hyderabad 500 007

Genetically modified or transgenic plants are created by the process of genetic engineering. Genetically modified plants can play a major role in revolutionizing the food production, nutritional quality, abiotic stresses in enlarging the crop area, post harvest traits, value addition, bioremediation, bioreactors and edible vaccines.

About 60 plant varieties 6 microorganisms have been deregulated. The field releases in 1947 were only (5) which has risen to 5102 in 1999 and upto April, 2000 the releases were 2474. Most frequent categories of field released genetically modified (GM) plants reported are herbicide tolerant 1853 (29.2%), insect resistant 1595 (24.5%), product quality 1195 (18.3%) viral resistant 650 (10.0%), agronomic 385 (5%), fungal 319 (4.9%) and others 529 (8.1%) upto April, 2000

In terms of Global area, about 40 million hectares or 100 million acres have been covered by transgeneics mostly in USA, Argentina, Canada and China making all out efforts to increase the transgenic acreage and cropping pattern. The Industrial countries dominate the scene, about 32.8 mill. Ha (82%) of transgenics are grown, where as developing countries contribute to only 7.1 mill. Ha. 18%. Soybean was is the major transgenic crop grown in 21.6 mill. Ha. (54%), followed by corn 11.1 mill. Ha. (28%), cotton 3.7 mill. Ha. (9%), canola 3.4 mill. Ha. (9%).

Genetically modified plants have been developed for about 200 traits in 60 plant varieties including protein energy malnutrition, nutritional anemia caused by iron deficiency and vitamin A deficiency involved in vision impairment.

Genetically modified crops under commercialization for improved trait include maize, cotton, canola, soybean for herbicide tolerance besides quality traits. Transgenic tomatoes for delayed ripening high solids, high lycopene and potato for higher starch, nutritious proteins, antibrowning etc. are under commercial cultivation.

India has made remarkable progress since independence . Population has trebled, food grain production has increased four fold. Food security is still a major problem to feed the growing millions due to limited land resources. Despite all the advances, at least 800 million people in the world are undernourished of which about 200 million are in India mainly due to lack of purchasing power.

Gene manipulation through biotechnological approaches is the hope of the future and will provide an unlimited opportunity for meeting the expectations of third world people/year added mostly in the poorest countries. The lecture will be illustrated with specific examples.

11

CALCIUM, THE CELL CYCLE AND DIFFERENTIATION IN *DICTYOSTELIUM DISCOIDEUM*

VIDYANAND NANJUNDIAH

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In the soil amoeba *Dictystelium discoideum*, differentiation follows the aggregation of a large number of seemingly identical starved amoebae. It has long been believed that the differences that appear between one cell and

another must be on account of differing spatial locations in the multicellular 'embryonic' structure. However, recent experiments support another old belief, namely, that differentiation builds upon pre-existing micro-heterogeneities between the amoebae that form a single aggregate. This talk will present evidence that cell-to-cell variations in calcium and cell cycle phase at starvation are two early inputs that enable us to distinguish between the fates of different cells.

12

SIGNAL INTEGRATION IN HUMAN CANCER PROGRESSION

SUDHIR KRISHNA

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Invasive cervical tumors, a major subset of human epithelial neoplasms, are characterized by the consistent presence of papillomavirus oncogenes 16 or 18 E6 and E7 products. Three of the four key events required for human epithelial transformation – activation of telomerase, inactivation of the Rb /p16 pathway and inactivation of the P 53 protein– are achieved through functions of HPV E6 and E7 oncogenes. Consistent with a key role for activated Ras signaling in transformation of immortalized human epithelial cells, activated Ras alleles complement HPV oncogenes. Ras mutations are found at a relatively low frequency in human cervical tumors.

The Notch family of transmembrane receptors is a major regulator of cell fate determination and has also been implicated in tumor progression. However, the role and regulation of Notch signaling in epithelial tumors, which constitute the majority of human neoplasms, is poorly understood. Recent reports reveal that cervical tumors consistently exhibit cytosolic and nuclear forms of Notch1, suggesting the possible persistent activation of the Notch pathway in these tumors. In this study, we show that Notch1 activation synergizes with papillomavirus oncogenes in transformation of immortalized epithelial cells. A major consequence of Notch signaling in these cells is the acquisition of resistance to anoikis, an apoptotic response induced on matrix withdrawal. This resistance to anoikis by activated Notch is mediated through the activation of PKB / Akt, a key mediator of survival in diverse systems, revealing a novel link of Notch signaling with survival

pathways . Previous experimental models have suggested that only truncated activated alleles of Notch signaling with survival pathways. Previous experimental models have suggested that only truncated activated alleles of Notch genes can be oncogenic. We show the Notch1 ligand, Jagged1, is expressed in the transition to invasive human tumors and in cell lines generates resistance to anoikis and sustains transformation. We propose that ligand dependent Notch signaling sustains papillomavirus mediated epithelial tumorigenesis and substitutes for the Ras pathway. Modulating Notch function offers novel therapeutic strategies.

13

THE EVOLUTION OF CO-OPERATION AND ALTRUISM IN A SOCIAL WASP

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In social insect colonies, one or a small group of individuals (queen/s) monopolize reproduction and the remaining (workers) perform various tasks required for the welfare of the colony and for successful reproduction by the queens. The evolution by natural selection of such co-operating and altruism on the part of workers remains a major unsolved problem in evolutionary biology. Hamilton's rule provides a powerful conceptual framework for investigation of this phenomenon. Primitively eusocial polistine wasps provide equally powerful model systems for empirical investigations. I will describe our theoretical and empirical studies using the primitively eusocial wasp *Ropalidia marginata*, which suggest a weak role for genetic relatedness but strong roles for ecological, physiological and demographic factors in the evolution of cooperative nesting and altruism. A simultaneous consideration of genetic, ecological, physiological and demographic factors that influence the inclusive fitnesses of solitary nest foundresses and workers, permits the prediction that only about 4% of the individuals in a population should prefer the solitary nesting strategy. In striking confirmation of this prediction, empirical investigations demonstrate that 4.6 to 5.7% of *R. marginata* females choose to initiate single foundress nests and 94.3 to 95.4% choose to nest in groups.

14

BASIC GENETICS FOR THE OBSTETRICIAN

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The field of human cytogenetics has been a boon to medical practitioner in the light of improved cell culture techniques and a series of chromosome banding techniques including, *in situ* hybridization and chromosome differential banding has enabled to delineate various chromosomal structural anomalies like, deletions, additions, inversions, translocations, etc. The latest techniques of chromosome painting allows one to accurately identify gene loci of interest. A Fluorescent In Situ Hybridization (FISH) is the new molecular cytogenetic technique that combines the advantage of DNA specificity with direct microscopic visualization of metaphase chromosome spreads, interphase cells or whole tissue sections fixed on microscopic slides. As such, application of these techniques on human material elicit fetal sexing, aneuploid detection in interphase cells and characterization of many chromosomal syndromes and pre-implantation diagnosis of genetic disorders using polar body or blastomere biopsy and further, prediction of severity, prognosis and predisposition in malignancies like chronic myeloid leukemia, breast cancer etc. The timely application of many such techniques will no doubt add much importance to genetic counselling.

15

BIOLOGICAL CLOCKS IN BATS < MICE AND HUMANS.

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Of the researches being reported here, the findings on the 'Social synchronization' of circadian rhythms in the flight/rest activity of an insectivorous rhythms in the locomotor activity of pups of the field mouse *Mus booduga* are first reports of their kind. Some of our data on human circadian rhythms are also new in principle.

BATS :

A colony of about 500 bats of *Hipposideros speoris* inhabits in clusters

of bats in the pockets of natural cave 15 to 40 m from the cave mouth. The bats experienced a constant temperature of 27° C and invariant relative humidity were no clues to signal day or night. Yet the entire colony flew out 5-10 Min after sunset. Flight activity experiments performed on bats held captive 40m deep inside this cave revealed that free-flying conspecifics of the colony were 'socially entraining /synchronizing' the activity/rest cycles of the captive bats (which has no access to light / dark cycles) This social synchronization appears to be species specific . The cave complex is situated ca 8 km away to the east of the Madurai Kamaraj University campus (9 58' N lat ; 78 10' E long) .

MICE :

In the field mouse *Mus booduga* the mother conveys the information of day/night behaviourally by means of presence /absence cycles (PA cycle) to her pups. Mother's presence indicated subjective day and absence indicated subjective night . We called this 'postpartum maternal entrainment' Such entrainment was possible only when the mother is present for a minimum of 8h (PA 8: 16h) and not exceeding 16 h (PA 16 : 8h). The pups entrained to PA cycles of 11.5 : 11. h, 12 : 12 h and 12.5 :12.5 h, but NOT to 11 : 11 h and 13 : 13 h These values of T= 23 h and T=25 h, therefore describe the "limits of maternal entrainment".

HUMANS :

Thirteen human subjects (4 females and 9 males) of age 20-35 years were studied for their sleep /wake cycles, rectal temperature profile, meal timings, blood pressure, short interval estimation, alertness etc in a 'human isolation facility' 25' x 25' specially built for the purpose. The circadian rhythms in these functions free-ran with periods longer than 24 h. In all instances, the subjects in socio-temporal isolation 'underestimated' time, in some cases very steeply. We reported for the first time that the menstrual cycle in the human female is not coupled to the sleep/wake clock. The 2 h interval estimation by the experimental subjects itself expanded and contracted 'like a time systole' as a function of the duration of wakefulness. In four marathon experiments the rectal temperature rhythms and sleep/wake rhythms internally dissociated resulting in novel sleep / wake correlations. All experiments were carried out by me and my students in the Department of Animal Behaviour & Physiology, School of Biological Sciences, Madurai Kamaraj University.

BIOCHEMICAL APPROACH TO DIAGNOSIS AND MANAGEMENT OF INBORN METABOLIC DISORDERS

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The recent spurt in knowledge of human genomics and molecular biology of genetic disorders has added new dimensions to the diagnosis and possible therapeutic/preventive measures to some of the rare inborn metabolic disorders (IMDs). Though the DNA based molecular probes and the prospectus of gene therapy is widely discussed, given the complexity in terms of varieties and often overlapping clinical manifestations, the diagnosis of IMDs still remains a challenge. While the diagnosis based on DNA probes relies on the findings of mutation of suspected gene, the biochemical approach to diagnosis of IMDs entail the assessment of functional integrity of suspected metabolic pathway (s) meaning the assessment of the gene product (protein) at functional level. The precise diagnosis of IMDs can be best accomplished by combined expertise of phenotyping the disorder by clinicians and laboratory back up by biochemists. Screening of clinically suspected subjects with simple urine tests based on chemical methods and routine blood chemistry followed by measurement of specific metabolites and assay of the relevant enzymes confirm the diagnosis in most cases. During the years 1994 – 2000, among the 8,567 cases referred to our department, a total number of 258 (3%) cases of various IMDs, which included carbohydrate metabolism (n=152), sphingolipidoses (n=55), aminocidopathies (n=44), mucopolipidoses (n=3), and two cases each of purine and porphyrine metabolism, were confirmed. Diagnosis in turn was useful in administering therapeutic/preventive intervention by way of dietary manipulation /vitamin supplements and /or genetic counseling. The relative low rate of confirmed diagnosis is attributed to the possible over referral due to lack of expertise in clinical phenotyping and inadequate laboratory facilities to carry out a varieties of metabolic work up, particularly in the area of organic acidemias/ acidurias. Considering the population and ethnic diversity of our country, a referral centre for IMDs of national character with a network of regional centers for would be of immense use to tackle the diagnostic dilemma of IMDs as a group of genetic diseases

KARYOLOGICAL STUDIES IN SIX SPECIES OF *ANTHURIUM* SCHOTT

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Karyological studies on 6 species of *Anthurium* Schott are presented. The karyotypic information provided for all the species forms a new and original contribution to the extant information, considerable variation exists in chromosome size among the species studied. A diploid number of $2n=30$ ($x=15$) has been recorded in 5 species among the 6 species studied, $2n=38$ was recorded in *A.hoffmanii*, the results of the present study confirmed $x=15$, most common. However, each of these taxa has certain chromosomal feature of marker value and therefore could be identified on the basis of karyomorphology, which would be useful in understanding their interrelationship, as well as in breeding program.

Species of *Anthurium* Schott belonging to the family *Araceae* were distributed in the tropical regions of America ranging from northern Argentina to Mexico. The genus comprises terrestrial and epiphytic rain forest plants. Despite the large size of the genus, cytological information available was inadequate. Some of the chromosome counts were conjectural and need confirmation in view of the older techniques employed by earlier workers. The significance of the presence of β -chromosomes in several species was yet to be understood. In view of the importance of such significant information in understanding their phylogeny, interrelationship, taxonomy and also their utility in improving programs, the present investigations deal with 6 species *A. grande*, *A. olfersianum*, *A. pedato-radiatum*, *A. warocqueanum*, *A. hoffmanii*, *A. pentaphyllum* of the genus, which were of horticultural interest. Chromosome numbers were available for only a little over 100 species of about 600-800 species known in the genus (Croat 1980).

PUFFING OF THE TELOMERIC Q-BAND IN THE CHROMOSOMES OF A PLANT, *LATHYRUS SATIVUS*

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Recent research has brought out the significance of telomeres which also possess genes. The shortening in the length of telomeres after each mitotic cycle, during DNA replication, is an established fact, which is compensated and restored in the healthy young dividing cells. The process is being catalysed by telomerase. The presence of telomerase and genes in the telomeric region may have relevance with puffing of the telomeric Q-band. It is for the first time that puffing of the telomeric Q-band is being reported in the chromosomes of a plant, namely, *L. sativus* L.

19

SPONTANEOUS BINEMIC SPIRAL SOMATIC CHROMOSOMES OF *CRINUM LATIFOLIUM*

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As a rule, the somatic chromosomes do not show spiral structure and are uninemic, that is, double in prophase and metaphase, and single in anaphase with replication during the intervening interphase. But, spirally visible double anaphase and four stranded metaphase chromosomes, observed spontaneously in the root tips of *Crinum latifolium* L, establish their binemic nature. It is an exception, to the fact that a single chromatid is the unit of eukaryotic chromosome, thereby, reviving the perpetual controversy between uninemy versus polynemy.

20

CYTOLOGICAL STUDIES IN DIFFERENT INDIGENOUS ACCES- SIONS OF *ALLIUM SATIVUM*

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Allium sativum Linn (Garlic) is a popular condiment for seasoning a wide variety of dishes. It has attracted the attention of many cytologists for reasons of plasticity of its chromosome complement. Cytological studies were carried out on 17 indigenous accessions of garlic. All the accessions revealed uniformity in chromosome number $2n=16$. But each accession is different from the other in respect to its chromosome length, ACL, TCL values, F%, TF% and karyotype formula. Heteromorphism has been ob-

served in eight accessions. Seven accessions possessed it on the eighth pair of the chromosomes and one accession of the sixth pair. The occurrence of heteromorphism is not unexpected in vegetatively reproducing taxa. It is attributed to structural alterations. Barring mutation, it is the only source of variation in garlic. Satellite (SAT) chromosomes are cytological markers which enable to understand the morphology of the chromosomes. SAT chromosomes have been observed in 5 accessions. Normally it is observed in the short-arm of the sixth and seventh pairs of the chromosomes. But in the present investigation it has been observed on other pairs of chromosomes i.e. 2,3,5 or 8. One accession possessed SAT on the long-arm whereas four accessions possessed it on short-arm of the chromosomes. Variation in the number and position of the SAT on other pairs of chromosomes have also been reported in other species. It has been found that there is no consistency in the position of SAT chromosomes for a particular pair. This nature is attributed to repatterning of the chromosomes. Absence of SAT in other accessions revealed deletion of the segment carrying it and more over they are susceptible of natural mutations. Variability in the number and position of SAT provides additional cytotaxonomic characters.

21

RADIATION INDUCED TETRAPLOIDY IN *CAPSICUM ANNUUM* L

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Fourteen tetraploids were isolated in M2 generation raised from Gamma-ray induced selfed progeny of M1 semisterile of a cultivar x 235 of *Capsicum annum*. All the tetraploids exhibited gigantism in exterior morphology over the corresponding diploid and the progenitor M1 semisterile. Detailed meiotic studies revealed the occurrence of chromosome associations such as I's, II's, III's and IV's, in them though their frequencies did vary. Meiosis was highly irregular with reduced chiasma frequencies in them. The binomial distribution test when applied for quadrivalent formation at metaphase-I revealed that the quadrivalent formation was non-random; mostly due to paucity of chiasmata and not due to lack of partner exchanges. The pollen sterilities were also very high. The reasons for reduced chiasma frequency and sterility in the tetraploids are discussed.

22

EVALUATION AND CYTOGENETIC MECHANISMS OF NUCLEAR-CYTOPLASMIC MALE STERILITY IN CHILLI (*CAPSICUM ANNUUM* L.)

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Non -availability of stable nuclear-cytoplasmic male sterility (cms) in chilli (*Capsicum annuum* L.) is handicap in cms based hybrid development. During 1999, male sterile (CCA-4261) and maintainer (PBC-534) lines (variety Tumpang), were characterized for male sterility expression, fruit morphology and meiotic behaviour. Male sterility expression in CCA -4261 was found to be complete and stable over range of temperatures, therefore, PBC-534 has been considered as a potential stable maintainer. The fruit traits, viz., bigger size (9.2 x 0.9 cm), inverted -blunt apex and mild pungency associated with Tumpang, casted doubt in its direct utilization in developing F_1 s for green fruit. CCA-4261 has sporogenous male sterility, which also shares feature of functional male sterility because very little amount of stainable pollen are produced, which fail to release from the tetrad. Male meiotic analysis of CCA-4261 and PBC-534 plants revealed that in CCA-4261 meiosis was abnormal especially at T II (30% cells with laggard). These results have been explained in the light of non-release of pollen as a major and irregular meiosis (leading to little pollen formation) as an additional mechanism, which provides support to the former in relation to the complete expression of male sterility. Both these mechanisms detected at the cytological level are being re-examined through genetic analysis of fertility restoration.

23

OCCURRENCE, IDENTIFICATION AND PRELIMINARY CHARACTERIZATION OF GYNOECISM IN BITTER GOURD (*MOMORDICA CHARANTIA* L.)

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In bitter gourd (*Momordica charantia* L.), occurrence of gynoeious flowering habit is very rare. During the summer season, 2000, three

gynoecious plants designated as Gy-35, Gy-63 and Gy-263B were observed in three populations, viz., VRBT-35, VRBT-63 and IC-66263B, respectively. Two gynoecious plants (Gy-35 and Gy-63) were stable (produce only pistillate flowers) and the remaining one (Gy-263B) produced few staminate flowers at later stages. Seeds of five crosses involving gynoecious and selected male plants were developed and F_1 plants were evaluated (rainy season, 2000). The recovery of variable number of gynoecious plants in very small F_1 population, indicated that gynoecism is heritable and under the control of certain major genes. The unexpected segregation of sex forms in F_1 may be due to the existence of heterozygosity in male parents. The remarkable feature of the F_1 monoecious plants was significantly very high number of pistillate flowers ranging from 20% (Gy-263B x VRBT-63) to 50.2% (Gy-35 x IC-68263B) as compared to control i.e. 11.7% (Pusa Hybrid-2). Thus, materials generated during the study, have immense potential for the (i) study on genetics of flowering habit, (ii) development of gynoecious line and (iii) high yielding populations with ability to produce high pistillate flowers.

24

EFFECT OF GAMMA RAYS, EMS AND MMS ON BIOLOGICAL AND MUTAGENIC PARAMETERS IN CHILLI (*CAPSICUM ANNUUM* L.)

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The effect of Gamma rays, EMS and MMS were studied on various biological and mutagenic parameters in M_1 and M_2 generations of four popular chilli cultivars. Higher lethality for germination and seedling height and higher values for mutagenic effectiveness, efficiency, factor of effectiveness and mutants per mutation were noticed in EMS treatments of both individual and combined treatments. Among the four cultivars, the cultivar G4 and Byadagi produced more synergistic and less than additive effects. Similarly, G4 and Byadagi were found to be more sensitive than the other two cultivars K2 and CO-2.

BIOCHEMICAL CHARACTERISATION OF ALFALFA INDUCED MUTANTS

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Medicago sativa L. being a high protein forage crop, studies were planned to investigate the biochemical aspects of different promising M3 mutants of the plant in regard to the parameters of seed protein and the leaf protein content. In the present studies, eight M3 mutant lines induced by gamma rays, EMS, NMU and MHZ selected for their better performance, were analysed for their seed protein and leaf protein content. The biochemical analysis is a useful tool in understanding the basic architecture of an organism at the cellular and physiological level. In view of this, a study of leaf and seed protein content of the control and some of the promising M₃ mutant lines of alfalfa was undertaken in the present investigation. The various mutagenic treatments tried in the present work succeeded in inducing superior genotypes carrying beneficial alterations in regard to seed / leaf protein content. Such plant types deserve to be systematically tapped as a new plant resource carrying physiologically beneficial attributes.

THE MUTAGENIC EFFICIENCY AND EFFECTIVENESS IN *MEDICAGO SATIVA* L

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Medicago sativa L. popularly known as Alfalfa or lucerne is a member that belongs to the family Fabaceae. It is known as "Queen of fodder crops" of "Green gold". The plant is mainly used for cattle feed as hay, silage and pasture. The alfalfa hay is full of important ingredients like vitamin A, thymine, riboflavin, niacin, pantothenic acid, biotin, vitamin D and vitamin E. The chlorophyll can be extracted from the ground meal on a commercial scale and it comprises rich source of B carotene and xanthophylls. For the

induction of mutations, different mutagens like gamma rays, ethyl methane sulphonate (EMS), N-nitroso-N-Methyl urea (NMU), and maleic hydrazide (MHZ), were employed in case of variety T9 of *M. sativa* L. The chlorophyll deficient sectors in the leaflets were of different types such as yellow (*xantha*), white (*albina*), yellow green (*chlorina*) and light green (*viridis*). These sectors were found at the apex, on the margins of leaflets or distributed throughout the lamina. In M2 generation, which was raised as progeny lines, a wide spectrum of chlorophyll mutations like *albina*, *xantha*, *chlorina* and *viridis* could be detected. From the data of the biological damage in M1 generation and frequency of the chlorophyll mutations in M2 generation, the relative effectiveness and efficiency of the four mutagens used was assessed. The values for each mutagen varied according to the M1 parameter taken for calculation.

27

QUALITATIVE ANALYSIS OF PROTEINS IN THE ROOTS AND NODULES (ROOT AND STEM) OF *SESBANIA SESBAN* (LINN.) MERRILL ON SDS-PAGE

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The protein banding patterns of roots have been compared with those of nodules (root and stem) of *Sesbania sesban* using Sodium Dodecyl Sulphate - Polyacrylamide gel electrophoresis (SDA-PAGE). The protein bands observed in nodules were different from that of roots. The nodule specific proteins associated by host genome, encoded by microsymbiont genome and transformation of bacteroidal cell in the bacteroids of *Sesbania sesban*.

28

ECOFRIENDLY CULTIVATION OF BRINJAL (*SOLANUM MELONGENA* L.) USING PLANT GROWTH PROMOTING RHIZOBACTERIA

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Continuous and indiscriminate use of inorganic fertilizers in many agricultural situations has resulted in degradation of soil health and productivity. Besides their high cost of production, the threat to ground water pollution is also a serious concern. Therefore, a need is felt in recent years to reduce the fertilizers input and encourage organic farming.

Many plant growth-promoting microorganisms colonize the root system of crop plants. In brinjal (*Solanum melongena* L.), one such association was isolated and identified to be *Bacillus polymyxa*. The isolated bacteria were tested for their ability to influence plant growth under field inoculated conditions. The plants were raised in 1X1 m nurseries (treated and control). The inoculum was prepared in nutrient broth and mixed with FYM before application. Thirty days old colonized seedlings were transplanted to the field plots. The plots received nitrogen and phosphorus fertilizers in reduced doses, which were 50% of the normal recommendation for brinjal. Results revealed that the treated plants at all levels showed significantly higher biomass, nutrient content and yield over their respective controls. The available nitrogen and phosphorus in the soil also increased. By this method of cultivation, the amount of nitrogen and phosphorus fertilizers could be significantly reduced and soil sustainability increased.

✓29

DEFENCE GENE EXPRESSION IN VIGNA RADIATA WILCZEK (L)

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The *Vigna radiata* Wilczek (L) is one of the important pulse crops of India. However, there are considerable yield losses due to disease caused by *Cercospora canasense* and *Rhizoctonia* sp. The attempts are being made to develop a resistance to these defence gene expression in susceptible and resistant cultivars. The expression of β 1, 3 glucanase and chitinase genes was studied. Similarly, the level of antimicrobial compound genestein was evaluated. The resistant and susceptible cultivars expressed the differential level of these compounds. The resistant cultivar showed the rapid and hypersensitive response, while in susceptible cultivars the response was slow and at low level. These responses can be correlated with resistant status of plant.

GENETIC EVALUATION OF SOME GLORY LILY (*GLORIOSA SUPERBA* L.) COLLECTIONS FOR SEED YIELD AND ASSOCIATED CHARACTERS

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Seventeen Glory Lily (*Gloriosa superba* L.) diverse germplasm were used to study the genetic variability for sixteen economic attributes. The GCV was observed high for days to sprouting, number of pods, seed yield, leaf area and number of leaves per vine seed yield per pod and number of branches per vine. The plant height, seed yield per vine, days to sprouting, number of leaves per vine, days to first flowering, days to 50 per cent flowering, number of pods per vine, number of seeds per pod, pod length, colchicine content, dry weight of pod, seed yield per pod, number of branches and leaf area per vine had higher heritability estimates. Whereas, leaf area and number of leaves per vine, days to sprouting, number of pods and seed yield per vine recorded higher Genetic Advance (GA) coupled with higher heritability indicating that it is controlled by additive gene action. Thus, phenotypic selection on the basis of these traits may be effective for its yield improvement.

INTERSPECIFIC HYBRIDISATION IN *CAJANUS* THROUGH CONVENTIONAL AND IN VITRO METHODS

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In spite of substantial improvement in the Pigeon+pea breeding programmes, the cultivars are still suffering from disastrous effects of susceptibility to pod+borer, *Fusarium* wilt and phytophthora blight diseases and to abiotic stresses. Some of the wild species of *Cajanus* possesses many desirable traits which are not available in pigeon pea gene pool. Hence, introgression of the desirable genes from wild to the cultivated variety could be achieved through interspecific hybridisations by conventional and *in vitro* methods. Four of the wild species, viz ; *C. cajanifolius*, *C. platycarpus*, *C. scarabaeoides* and *C. sericeus* were used as donor parents in the reciprocal crosses with *C. cajan*. For overcoming post zygotic barriers, *in vitro* methods

were tried for rescuing the immature embryos of problematic interspecific crosses. The immature hybrid embryos of 11-20 day-old are ideal for obtaining plantlets. The different *in vitro* methods tried and results obtained would be discussed.

32

GERMPLASM EVALUATION AND INDUCTION OF VARIABILITY IN COLEUS (*COLEUS PARVIFLORUS* BENTH.)

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Coleus (*Coleus parviflorus* Benth.) is an important minor tuber crop grown extensively as a vegetable in most of the homestead gardens of southern India. The aromatic essential oils α thujone and β farnescene present in tubers confer medicinal properties to the tubers. Sixty accessions of *coleus* collected from different ecogeographical regions of India were grouped into ten clusters using principal component analysis. Clusters included genotypes from different geographical regions which infers that factors other than geographical diversity might be responsible for such grouping and that there was no parallelism between geographical distribution and genetic diversity. The germplasm evaluation showed high genetic variability in most of the yield attributing characters except days to flowering and days to tuberization. Among the tuber characters, volume and weight / tuber had the highest value for heritability and moderate values for phenotypic coefficient of variation. Mutants derived from the selected genotypes representing the clusters showed higher variability for tuber yield and its attributes. The chemical mutagen (EMS) was more effective in inducing variability compared to physical mutagen (gamma ray).

33

GENETIC DIVERSITY OF SEED OIL PARAMETERS IN SOME SPECIES OF *SESAMUM* (PEDALIACEAE)

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Seed oil content, free fatty acids, saponification value, iodine number and fatty acid composition in cultivated sesame, *Sesamum indicum* and wild species namely, *S. alatum*, *S. laciniatum* and *S. schinzianum* have been studied. In diploid species, oil content ranges from 54% in *S. indicum* and

33% in *S. alatum*. In tetraploid species, *S. laciniatum* it is 25% and octaploid species *S. schinzianum* contains 21% oil. Seed oil of above species exhibit diversity with regard to free fatty acid content, saponification value and iodine number. Analysis of methyl esters of seed oil reveals that the major fatty acids are palmitic (C_{16}), stearic (C_{18}) and arachidic acid (C_{20}) and their proportion is 10, 5 and 1 % respectively. Unsaturated fatty acids constitute the major proportion and the principal unsaturated fatty acids are oleic ($C_{18:1}$) and linoleic acid ($C_{18:2}$) which are present in equal proportion. Among unsaturated fatty acids, linoleic acid is an essential fatty acid and its higher proportion in the oil is a desirable quality character. Linoleic acid content is 36.11% in *S. indicum*, 38.54% in *S. alatum*, 48.34% in *S. laciniatum* and 50.15% in *S. schinzianum*. Present study reveals the genetic diversity in seed oil content and fatty acid composition. Sesame seed oil can be improved for quality by increasing linoleic acid content through hybridization and further selection with its wild relatives.

34

INTERACTION BETWEEN SPIKE DEVELOPMENT AND INTER-NODE ELONGATION IN BARLEY

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Dwarfism in barley has been studied in considerable detail by utilizing a large number of erectoides, dwarf and semidwarf mutants. However, not much information is known about the interaction between spike and (culm) internodes. Therefore, the interaction between spike development (spike length, spike nodes and no of spikelets) and internode elongation (length of individual internodes and culm length) was studied using six gamma ray induced, true breeding, reduced height mutants in barley (cv. K-169). In these mutants viz., dwarf, semidwarfs, early maturing, chlorina and lax panicle types, the height reduction is associated with either earliness, spike alteration or impairment of chlorophyll synthesis. The length of internodes are correlated with one another and to culm length and spike traits. The length of an internode is positively correlated with the length of other internodes but significant association was noticed only with the adjacent internode. The length of first internode from top (That supports the spike) is positively and significantly correlated with second and third internodes (from top) but not with the lower (basal) internodes. There is significant positive correlation between spike length and culm length ; spike length

with other spike traits (spike nodes and no. of spikelets); spike nodes with no. of spikelets and culm length. On the other hand, culm length showed significant positive correlation with the top four internodes only. The no. of spikelets also showed a positive and significant association with internode length, but with the two top internodes only, and thus suggests that panicle development affects the upper internodes. The results also indicate that reduction in culm length has negative effect on spike development with reduction in spike length, spike nodes and no. of spikelets.

35

GENOME SIZE VARIATION IN *DALBERGIA LATIFOLIA* ROXB (FABACEAE)

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Intraspecific genome size variation in 20 genotypes of *Dalbergia latifolia* covering its distribution range in western ghats of Karnataka has been studied through Feulgen cytophotometry. *D. latifolia* is an exclusive diploid taxon with $2n=2x=20$ chromosomes. Mean 4C DNA amount varies from $6.824 \pm 0.0035\text{pg}$ to $6.902 \pm 0.0016\text{pg}$. Difference of 1.13% genome size variation is apparent between lowest and highest DNA values. ANOVA test reveals that the genome size variation at intraspecific level in this species is non-significant. Thus, genome size in all the accessions of *D. latifolia* is stable with no significant variation.

36

GENETIC PARAMETERS IN RESPECT OF GROWTH AND YIELD TRAITS IN CHILLI (*CAPSICUM ANNUUM* L.) UNDER RAINFED AND IRRIGATED CONDITIONS

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Genetic parameters like variability, heritability and genetic advance as per cent mean were studied for various growth and yield traits of sixty chilli genotypes under rainfed and irrigated conditions at Gandhi Krishi Vignana Kendra, Bangalore during 1993-94.

The differences between phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) was relatively narrower with respect

to plant height, number of branches and spread of plant under rainfed conditions than under irrigated conditions. For rest of the characters, a wide difference between PCV and GCV was observed irrespective of rainfed and irrigated conditions.

Higher broad sense heritability coupled with higher genetic advanced as per cent mean was observed for plant height, number of branches, spread of plant and days to 50 per cent flowering under rainfed conditions than under irrigated conditions. However, final whole plant dry weight showed higher heritability under both rainfed and irrigated conditions. Rest of the characters manifested lower heritability coupled with lower genetic advanced as per cent mean.

✓ 37

BIOSYSTEMATIC STUDIES IN INDIAN SQUILL

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Systematic and detailed phytochemical and cytological screening have been made in different populations of Indian squill which is used as a cardiac drug, as an anti-cancer agent, in curing rheumatism pneumonia etc. Phytochemical studies of bulb extract revealed variations within populations of *U. indica*. The results are recorded and discussed.

Quantitative C-band karyotyping and DNA content determinations were performed. The populations differ strikingly in their banding patterns and in their DNA content.

The present study is an attempt to discuss the above result. Our article is an investigation aimed at making Indian squill an economical and medicinally important crop for India.

✓ 38

CHROMATOGRAPHIC DISTRIBUTION PATTERNS OF FLAVONOIDS IN UROCHLOA P. BEAUV (POACEAE) AND THEIR TAXONOMIC SIGNIFICANCE

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Chromatographic distribution patterns of flavonoids in leaf extracts of eight taxa of *Urochloa* P. Beauv., panicoid grasses of fodder importance, were studied employing two dimensional paper chromatography. Of the total 23 flavonoid spots recorded, eight spots were common and range was 11-17 spots in different taxa. The degree of relationship between the taxa was measured with paired affinity index values and depicted in dendrogram. The four varieties of *Urochloa panicoides* P. Beauv. Var. *panicoides*, var. *pabescens* (Kunth) Bor, var. *marathensis* (Henr.) Bor and var. *velutina* (Henr.) Bor showed very close affinity between themselves and differ widely with the others species. *U. oligotricha* (Fig. And De Not.) Henr. Wit maximum number of 17 spots showed distinct pattern of flavonoids. The chromatograms of *U. mosambicensis* (Hack.) Dandy almost overlaps with that of *U. pullulans* Stapf. The chromatogram of *U. trichopus* was distinct and showed more affinity with that of *U. mosambicensis*. There relationships are discussed in view of solving the taxonomic existing between these taxa.

39

BIODIVERSITY IN RELATION TO GENETIC DIVERSITY IN THE FAMILY CUCURBITACEAE

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Biodiversity has been the result of three billion years of evolution involving mutation, recombination and natural selection and genetic diversity. Changing environment has a large bearing on the evolution of new species and also extinction of others. Hence, genetic diversity clubbed with ecological diversity constitute the biological diversity. Further, genetic diversity is the amount of genetic variability among individuals of a single species and also between species.

The family cucurbitaceae consisting of 90 genera and 750 species in which 110 species belonging to 36 genera were reported in India. In India, about 16 species belonging to 11 genera are widely cultivated. The members of this show a great deal of genetic diversity due to their outbreeding and adaptibility to different ecological conditions. Lost of the annual species of the genera like *Cucurbita*, *Bryonopsis*, *Legnaria* are relatively insensitive to photoperiod, whereas, species of *Trichosanthes*, *Momordica*, *Melothria*, *Cucumis* and *Citrullus* are sensitive to photoperiod. Some of the members of the family show resistance to drought, whereas some of the members are disease resistant. This further facilitates to a significant extent in profusion

of genetic resources. Therefore, the conservation of biodiversity for this family is essential as it is a staple food in India and to make resources more productive with ecological damages which requires proper investigation from this angle. The present work was undertaken to have a resource inventory, region by region and detail analysis of the collected species (cytological, genetical and morphological) to maximise production with new cultivars on a sustainable basis. The present studies pertain to the available species of Gangetic diara land and also from the places of North Eastern region.

40

IDENTIFICATION OF NECROSIS AND CHLOROSIS GENES IN INDIAN HEXAPLOID AND TETRAPLOID WHEAT VARIETIES

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Ten varieties each of hexaploid wheat (*Triticum aestivum*) and tetraploid wheat (*T. dicoccum*) were crossed to four tester hexaploid wheat cultivars, Sujatha ($Ne_1ne_2 Ch_1ch_2$), C 306 ($Ne_2Ne_1ch_1Ch_2$), Kharkof ($ne_1Ne_2 Ch_1ch_2$) and Sonalika ($ne_1Ne_2 ch_1Ch_2$) to determine the genotypic status of chlorosis and necrosis genes in hexaploid and tetraploid wheat cultivars. Among the ten hexaploid wheats, six of them were found to carry necrotic gene Ne_2 , two cultivars carrying the Ne_1 gene, while the other three were non-carriers. All the hexaploid wheat varieties were found non-carriers for chlorosis. Among the ten tetraploid wheats, seven were found to carry both the necrosis gene Ne_1 and the chlorosis gene Ch_1 . Three varieties were found to be non-carrier for necrosis and chlorosis genes. Allelic variation at the Ne_1 (w,m,s), Ne_2 (w,wm, m, ms, s) and Ch_2 (s, m) were noticed.

✓41

TRANSFER OF SPECIFIC GENES FOR RUST RESISTANCE INTO INDIAN HEXAPLOID WHEAT CULTIVARS

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Five stem rust resistance genes (Sr24, Sr25, Sr26, Sr27 and Sr31) and three leaf rust resistance genes (Lr19, Lr24, Lr26) and one stripe rust resistance gene (Yr9), present either singly or in combination, were transferred from hexaploid wheat stocks into three Indian wheat cultivars namely

PBW 1626, VL 738 and Raj 1555. The near --isogenic lines were constituted in BC2F5 and BC5F5 generations. Constituted lines were screened against individual rust races at seedling stage and at adult plant stage. Immune to moderately resistant reaction at seedling stage and highly resistant reaction at adult plant stage were recorded. Yield trials under rust free condition revealed that the near-isogenic lines in BC2F5 showed reasonably very good agronomic characteristics, however, the seed quality was very poor. Hence, final selections were made in BC5F5 lines. Lines carrying stem rust resistance genes Sr25+Lr19 showed superior performance in all the 3 wheat genetic backgrounds, while Sr31+Lr26+Yr9 gene complex showed yield reduction in all the three wheat stocks. Based on the seed quality and yield performance, nine lines were constituted for commercial purpose and six lines as genetic stocks.

42

EVALUATION OF 2, 4-D AS MALE GAMETOCIDE ON *PHASEOLUS AUREUS* ROXB AND A NEW METHOD OF PLANT BREEDING

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A gametocidal compound may be generally defined as a growth regulator that inhibits gamete development. The reasons for the sterility induced by chemical treatment have not yet been thoroughly investigated.

Phaseolus aureus Roxb. Var. J-781 mung is one of the most highly esteemed and prized pulses of India. 2, 4-Dichlorophenoxy acetic acid is one of the gametocidal or pollinocidal compounds which is commonly used to induce pollen sterility in plants. However, because of its dual function as auxin and herbicide, responses to sub-lethal levels are frequently of different nature.

Pollen of the series of successive flowers used : F, F-24, F-28, and F-72 series *i.e.* open flowers and the flower buds which require 24, 48 and 72 hours to open respectively. Pollen viability was tested by using 2, 3, 5-Triphenyl-tetrazolium chloride (Hauser and Morrison 1964). Viability counts were taken at weekly intervals after treatment for the first 6 weeks. Germination of pollen grains of successive flowers was studied by standing - drop technique in an optimum concentrations of sucrose (which was 10% sucrose for F-24 series, 20% for F and F-48 series and 30% for F-72 series). The pollen grains were incubated soon after the dehiscence of

anthers (in open flowers) and observations were made after 24 hours of incubation. The data was statistically analysed applying 't' test.

All the concentrations of 2, 4-D above 600 $\mu\text{g/ml}$ prevented flowering permanatly. All the concentrations of 2,4-D above 600 $\mu\text{g/ml}$ caused 100% mortality after one week of treatment . Hence , 800 $\mu\text{g/ml}$ 2,4 -D confirmed the lethal dose for *Phaseolus aureus*.

In the present investigation, higher percentage of pollen germination was noted in F-24 and F-48 series than in F series. This proves that the pollen of successive flowers are an ideal for pollen storage and its subsequent use in plant breeding programmes. Also, maximum reduction in the pollen viability ($14.07 \pm 0.11\%$ against $85.60 \pm 0.49\%$ viability in control) was recorded in F-72 series after 5 weeks of treatment of 600 mg/ml 2,4-D. An increase in the time interval between the treatment and the observation of sterility count, decreased the percentage of pollen sterility or even sometimes normalised (equal to that found in control). After 8 weeks of treatment $22.75 \pm 0.16\%$ pollen viability was noted in the same series and concentration of 2,4-D. For the successful plant breeding it is necessary that the cent percent pollen fertility should be suppressed and it should be retained for the longer period. Thus it is very clear that the method of chemical induction of pollen sterility is useless for the sucessful plant breeding programme. It should be pointed out that all the concentrations of 2, 4 -D above 200 $\mu\text{g/ml}$ permanently suppressed the germination of pollen in all the 4 series investigated. The significance of the results shall be discussed.

✓ 43

MALE STERILITY INDUCTION RED MISSILE BY MALEIC HYDRAZIDE

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Present paper deals with the effect of 10-10-50, 75, 100 ppm maleic hydrazide (MH) on pollen fertility of successive flowers (viz. F, F-24, F-24, F-48, F-72 series i.e open floweers and the flower buds which require 24, 48, 72 hours to open respectively) of red missile cultivar of *Capsicum frutescens* L. Foliar applications of different concentrations of MH were made when the crop started uniform flowering. Fertility counts were taken at weekly intervals after treatments for the first 10 weeks. Pollen fertility of successive flowers was estimated in acetocarmine preparations.

Foliar application of 10 ppm maleic hydrazide caused 18, 17, 15, 15% pollen sterility in F, F-24, F-48, F-72 series respectively after one week of treatment. However, the treatment of 100 ppm MH resulted in 41, 40, 37, 35% pollen sterility in F, F-24, F-48, F-72 series respectively when the observations were made after one week of treatments. An increase in time interval between the treatment and the observations of sterility count, decreased the percentage of pollen sterility. This is further supported by the differential pollen sterility formation in successive flowers. This is because the effect of the sprayed chemical is nullified with the lapse of time interval. As a result of which the pollen sterility is reduced or even normalized (equal to that found in control i.e. 15% in red missile). Pollen sterility is normalized in F series after 2,3,4,6,8 weeks of treatments of 10, 20, 30, 40, 50% MH respectively. However, 1, 1, 1, 2, 6, 8 weeks are required to normalize the pollen sterility in F-72 series treated with 10, 20, 30, 40, 50, 75 ppm MH respectively. Even after 10 weeks of treatment of 75 and 100 ppm MH 17 and 20% pollen sterility respectively was noted in F series, while 16% pollen sterility was recorded in F-72 series treated with 100 ppm.

Present investigation also proves that the pollen of successive flowers acts as an ideal indicator of pollution.

44

EVALUATION OF MALEIC HYDRAZIDE AS MALE GAMETOCIDE ON CLUSTER BEAN AND A NEW METHOD OF PLANT BREEDING

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Maleic hydrazide is very commonly used as gametocide as well as herbicide. Levi and Craft (1952), Molero and Balckhurst (1956) and Carroll (1957) have stated that MH does not show any residual effect on soil. However, the findings of the said workers are challenged by Salgare and Theresa Sebastian (1987) and Salgare (1997). Foliar applications of 5, 10, 25, 50, 100, 200-200-1000, 1000-1000-5000 $\mu\text{g/ml}$ MH was made on the 3 weeks old crop of *Cyamopsis tetragonoloba* Taub var. Pusa navbahar, Gawar, Cluster been (pre-flowering stage). After one week of treatment, the effect of MH pollen viability and germination of successive flowers viz. F, F-24, F-48, F-72 series i.e. open flowers and the flower buds which require 24,48,72 hours to open respectively. Pollen viability was tested by using 2,3,5-triphenyl tetrezolium chloride (Hauser and Morrison 1964). Pollen

germination was made in an optimum concentrations of sucrose (viz. 20% for F-24 and F-48 series and 30% for F and F-72 series). Pollen grains were incubated soon after dehiscence of anthers (in open flowers) and observations on pollen germination were made after 24 hours of incubation. The data obtained was statistically analysed applying 't' test.

Potentiality of pollen germinability was noted in all the 4 series. All the concentrations of MH above 400 $\mu\text{g/ml}$ prevented flowering. It should be pointed out that the higher percentage of pollen germination was noted in F-24 and F-48 series of successive flowers than F series. This proves that the pollen of the said series are ideal for pollen storage and their subsequent use in plant breeding indicating that the use of pollen of F series is not advisable as it is used. The treatment of the highest concentration which showed flowering produced 40.27 ± 0.39 , 40.00 ± 0.25 , 41.26 ± 0.32 , $42.38 \pm 0.17\%$ pollen fertility in F, F-24, F-48, F-72 series against 85.27 ± 0.45 , 85.20 ± 0.40 , 85.00 ± 0.56 , $85.36 \pm 0.30\%$ in control in F, F-24, F-48, F-72 series respectively. The significance of the results shall be discussed.

45

GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN RABI ONION (*ALLIUM CEPA* L.)

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Onion (*Allium cepa* L.) is one of the most important and popular bulbous vegetable crop grown commercially in India for local consumption and also for export purpose. There is an increasing demand for few varieties to suit consumer market. For a sound breeding programme, it is imperative to assess the relative magnitude of genetic variability, nature and extent of characters in association with yield and its related characters. The present study was carried out to assess genetic variability in terms of mean, GCV, PCV, h^2 , expected genetic advance as per cent of mean and path co-efficient, studied for yield and yield contributing traits in 15 genotypes of onion during 1999 *rabi* season.

The phenotypic coefficient of variation was higher than genotypic coefficient of variation in all the characters. But, the difference between the values of GCV and PCV was only marginal in all the characters including six yield related characters. This suggested the role of environment in the expression of genotypes. Heritability estimates were high for neck thickness, bulb equatorial diameter, per cent of A grade bulbs, doubles and bolters. In

spite of high heritability value for most of the traits, the expected genetic advance as per cent of mean ranged from 15.49 to 170.04. For most pairs of characters, the genotypic correlation co-efficient were higher than phenotypic correlation coefficient. Path coefficient analysis revealed that the maximum direct effect of yield was through average weight of bulb, per cent of A grade and B grade bulbs. The significant positive association was noticed between these characters which will be important for selecting high yielding genotypes. Hence, direct selection could be made for these characters for improving the yield.

46

HIMALAYAN PRIMULAS AND THEIR DIVERSITY IN CHROMOSOME LENGTH

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The members of the family Primulaceae is herbaceous plants occurring nearly in all continents especially in the north temperate and alpine regions of the world. There are reports of 98 species of Primulaceae in Nepal (Hara *et al.* 1978). This paper deals with the chromosome number and their length of *Primula* and its allied species *Androsace* and *Anagallis* dwelling in between subtropical to alpine region of Nepal Himalayas. Among these genera, the genus *Primula* is a larger member of the family, of which sixty-five species are found in Nepal. The basic number of chromosomes of *Primulas* are in dominant form. A remarkable variation in the size of chromosomes of the Nepal Himalayan *Primula* species is noted. It is also evident that majority of species have a specific area of distribution. Scarcely any species have been found growing both in the temperate and in the alpine regions. The high altitude dwellers exhibit relatively longer chromosomes than lower ones. The diversity in the absolute length of chromosomes in majority of the Himalayan *Primulas* shows a significant role in altitudinal adaptation.

47

STUDIES ON THE EFFICIENCY AND EFFECTIVENESS OF THE GAMMA RAY INDUCED MUTAGENESIS IN BHENDI

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An investigation was carried out to study the efficiency and effectiveness of the gamma ray in inducing chlorophyll and viable mutations in bhendi cv. Pusa Sawani and Parbhani Kranti. The M2 generation raised for another study was utilized for this investigation. The gamma ray treatments were 20, 40, 60 and 80 kR, besides a control was maintained in both the varieties. The selfed seeds of M2 generation were collected to raise the M3 generation and M1 seeds were selected for gamma ray treatments of 40, 50 and 60 kR as recurrent doses. In M1, all the treatments except 80 kR were utilized for recurrent treatment. The effectiveness for chlorophyll mutations ranged from 21.7 to 52.0 per cent in Pusa Sawani and 21.7 to 65.8 per cent Parbhani Kranti. The efficiency in terms of chlorophyll mutation was the highest at 60/40 kR on lethality in both the varieties, 40/40 kR in Pusa Sawani and 20/50 kR in Parbhani Kranti on injury and 40/40 kR in Pusa Sawani and 20/40 kR in Parbhani Kranti on sterility basis. The effectiveness for viable mutations ranged from 22.2 to 89.8 per cent and 27.8 to 85.5 per cent for both the varieties respectively.

48

ENHANCEMENT OF BIO-MASS THROUGH MULTIPURPOSE TREE SPECIES FOR SUSTAINABLE AGRICULTURE IN EASTERN DRY LAND TRACT OF KARNATAKA

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The role of agroforestry is indispensable in increasing the overall economy of the land, particularly growing of specific trees useful for various purposes is of utmost importance. Besides, this approach helps in improving the inherent qualities of the soil such as water holding capacity, and fertility status, prevention of soil erosion, providing fuel wood, green manure, fence poles, timber and forage all through the years. In this direction, selected species such as *Artocarpus heterophyllus*, *Azadirachta indica*, *Deris indica*, as border trees are already in practice in this tract. In the present study, three important species, *Acacia auriculiformis*, *Casuarina equisetifolia*, and *Grevalia robusta* were integrated with finger millet the later is an important dry land crop of this zone. The Biomass assessment over four years have shown significant increase of all the wood species. Furthermore, a comparative yield levels of sole crop of nagi over all these four years did not show any significant reduction in yield when it was from along with these four species. It is also observed that there was more than three times increase in biomass of all the three species. There is a possibility of

decrease in the yield of grains to an extent of 30 to 40 per cent after four years, which is attributable to competition for water and nutrients by tree species by their increased growth. Thus an integrated approach of agroforestry system not only provides an additional revenue but also provides better soil conditions, congenial for initial establishment and enhance the growth rate of multipurpose tree species.

49

THREE DIMENSIONAL KARYOTYPE ANALYSES OF CERTAIN SPECIES OF THE GENUS *SORGHUM* MOENCH

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Cultivated *Sorghum* is an important source of food and feed in many warm climate countries. Extensive taxonomic studies by earlier workers demonstrated the presence of extensive variability in this genus. Presently, ten species of *Sorghum* obtained from different countries, namely *S. ankolib* ($2n=20$), *S. bicolor* ($2n=20$), *S. dochna* ($2n=20$), *S. halepense* ($2n=20$ and $2n=40$), *S. hewisonii* ($2n=20$), *S. kafir* ($2n=20$), *S. milaceum* ($2n=40$), *S. plumosum* ($2n=20$), *S. purpureo-sericeum* ($2n=20$) and *S. verticilliflorum* ($2n=20$) were explored for their karyotype attributes using parameters like, arm's ratio, total length of the chromosome complement, centromeric index, gradient index, symmetry index, total chromatin length and total volume of the chromosomes and chromosome complements etc. The volume of the chromosome was calculated assuming a chromosome as two cylinders corresponding to two sister chromatids. The chromosomes were assorted into different categories on the basis of arm's ratio following Levan *et al.* (1964). These were further subdivided into different types, on the basis of total length of the chromosome. Although, these species possessed symmetric karyotypes differed significantly in total length and volume of chromosome complements.

50

INVESTIGATION OF MALE MEIOSIS IN 257 ACCESSIONS OF *CARTHAMUS* L SPECIES

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The genus *Carthamus* having about 25 species has been poorly explored cytogenetically. This genus included *C. tinctorius* an important oil

crop. Presently, while exploring and manipulating this genus cytogenetically, male meiosis was analyzed in 257 genotypes belonging to five species : *C. glaucus* ($2n=20$), *C. lanatus* ($2n=24$), *C. lanatus* sub-species *turkestanicus* ($2n=64$), *C. oxycantha* ($2n=24$), *C. palestinicus* ($2n=24$), and *C. tinctorius* ($2n=24$). These accessions were procured from several countries. Out of 257 accessions, 58 possessed significant amounts of meiotic anomalies. In these accessions, the course of both first as well as second meiosis was abnormal. The main types of meiotic anomalies included trans-cellular migration of chromatin between pollen mother cells, clumping of chromosomes at metaphase I and II, restitution nucleus formation during meiosis I and II, lagging of chromosomes during anaphase I and II, formation of micronuclei during telophase I and II, formation of chromatin bridges at anaphase I and II, etc. The abnormal courses of meiosis lead to the formation of monads, dyads, triads and polyads and executed significant amount of pollen sterility.

51

CYTOGENETIC EVALUATION OF SOME WILD SPECIES OF SORGHUM MOENCH FOR CHARACTERISING APOMIXIS

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For more than six decades, one of the most cherished dreams of plant breeders has been to find a way to transform food crops into super-plants able to reproduce without losing hybrid vigor, desirable agronomic traits or useful disease or insect -resistance. *Sorghum*, ranks third in the major food grain crops of our country. Apomixis has been discovered only in *S. bicolor* (L.) Moench. The frequency of apomixis in cultivated *Sorghum* is too low to be economically useful. A project has been currently undertaken for the detailed scanning and cytogenetic analyses of gramineous crops and their wild relatives for apomixis. Several cultivated as well as wild accessions of *Sorghum* are being explored for the presence of apomixis. This article deals with the cytogenetic evaluation of *S. helepense* Pers. ($2n=2x=20$ and $2n=4x=40$) and *S. miliaceum* Snowden ($2n=4x=40$). The tetraploid accessions of both the species exhibited anomalous meiotic course. Morphological analyses of large number of populations/accessions indicated the presence of high levels of natural introgression between these two species. In both these species apomixis manifested itself through facultative apospory.

CYTOMORPHOLOGICAL EVALUATION OF CADMIUM TOLERANT, PARTIALLY TOLERANT AND NON-TOLERANT GENOTYPES OF BARLEY

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Among the heavy metals, cadmium has raised the most concern because of its high toxicity, coupled with an exceptional tendency to accumulate in human beings. The genetics of heavy metal tolerance in crop plants has not been worked out. Presently, while working on this aspect, large numbers of accessions of different crops were screened for tolerance to several heavy metals including cadmium. This paper deals with the cytomorphological evaluation of certain cadmium tolerant, partially tolerant and non-tolerant genotypes of barley. Cadmium was given in the form of 10^{-3} M CdCl_2 solution. The parameters explored pertained to growth of seedling, root meristem cytology and male meiosis. Although, Cd treatment reduced significantly the radicle length of seven days old seedling of partially tolerant and non-tolerant genotypes, it could reduce active mitotic index and induce anomalies in the mitotic as well as meiotic course independent of the amount of tolerance present. Different types of cytological anomalies induced were related to chromatin agglutination, differential movement of chromosomes toward equatorial plate and poles of spindle apparatus, spindle breakdown and chromatin erosion and fragmentation.

ASSESSMENT OF CHROMIUM TOLERANT, PARTIALLY TOLERANT AND NON-TOLERANT GENOTYPES OF BARLEY

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Chromium, which has several roles in our daily life, is an essential element. This metal shows a wide range of oxidation states from -2 to +6. Studies have shown that Cr^{+6} compounds are approximately 100 times more toxic than Cr^{+3} compounds. Presently, while working out the genetics of heavy metal tolerance in crop plants, large number of accessions of different crops were screened for tolerance to several heavy metals including hexavalent chromium. The present paper deals with the cytomorphological evaluation of certain hexavalent chromium tolerant, partially tolerant and non-tolerant

genotypes of barley. Cr^{+6} was given in the form of $10^{-3}\text{M Na}_2\text{Cr}_2\text{O}_7\cdot 2\text{H}_2\text{O}$ solution. Cr^{+6} reduced significantly the radicle length of seven days old seedling of partially tolerant and non-tolerant genotypes. However, it reduced active mitotic index and induced anomalies in the mitotic as well as meiotic course of different genotypes independent of the amount of tolerance present. Different types of cytological anomalies induced were related to chromatin agglutination, differential movement of chromosomes toward equatorial plate and poles of spindle apparatus, spindle breakdown and chromatin erosion and fragmentation.

54

ANALYSES OF KARYOTYPE POLYMORPHISM IN BHABAR GRASS *EULALIOPSIS BINATA* (RETZ.) C. E. HUBBARD (POACEAE)

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Eulaliopsis binata (Retz.) C. E. Hubbard belongs to the tribe Andropogoneae, sub-family Panicoideae of family Poaceae and is commonly known as 'bhabar grass' in the tarai regions of Garhwal and Kumaun divisions (because it commonly grows on 'bhabar'-fans of the coarse gravel brought down from the hills). Since this grass has not been investigated earlier for its cytological and reproductive characteristics, this is the first report about the details of its karyotype. Samples of populations collected from six widely separated regions of Garhwal and Kumaun divisions were subjected to 3D karyotype analyses using several parameters including volume of the chromosomes and chromosome complements. The volume of the chromosome was calculated assuming a chromosome as two cylinders corresponding to two sister chromatids. The chromosomes were assorted into different categories on the basis of arm's ratio following Levan et al. (1964). These were further subdivided on the basis of total length of the chromosome. *E. binata*, having a chromosome number of $2n=20$ exhibited significant karyotype polymorphism.

55

KARYOTYPE STUDIES IN CERTAIN GENOTYPES OF *CARTHAMUS TINCTORIUS* L. OBTAINED FROM DIFFERENT COUNTRIES

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C. tinctorius, commonly called safflower, is the only cultivated species of the genus *Carthamus* L. This species is fast gaining importance as an oil crop. The present paper deals with the karyotype analyses of accessions procured from countries like China, Czechoslovakia, former Soviet Union, Portugal, Spain, USA and India. The karyotype analysis was carried out using parameters like, total length of the chromosome complement, centromeric index, gradient index, symmetry index, total chromatin length and total volume of the chromosomes and chromosome complements etc. The volume of the chromosome was calculated assuming a chromosome as two cylinders corresponding to two sister chromatids. The chromosomes were assorted into different categories on the basis of arm's ratio following Levan *et al.* (1964). These were further subdivided into different types, on the basis of total length of the chromosome. All the accessions possessed $2n=24$ and had symmetrical karyotype. However, the karyotype of various genotypes differed from each other in several parameters like gradient index, symmetry index, total chromatin length and total volume of the chromosomes and chromosome complements etc.

56

EFFECT OF TRIADIMEFON ON ANATOMICAL CHANGES IN LEAVES OF CHINA ASTER (*CALISTEPHUS CHINENSIS* L. NESS)

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Anatomical changes (in leaves) by using Triadimefon were studied in China aster. Aqueous solutions of Triadimefon (0.0, 1.00, 10.00 and 100 ppm) were applied on 20th, 30th and 20+30th days after planting. Observations were recorded on thickness of the leaf; palisade layer; number of layers in palisade tissue; length and breadth of palisade cells and spongy cells; and number of chloroplasts in spongy tissue.

Thickness of the leaf; Palisade layer; spongy layer; and average number of starch grains and number of starch grains in spongy cells were increased due to Triadimefon application as compared to control plants.

57

GENETIC ANALYSIS IN F1 HYBRIDS OF MARIGOLD

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Marigolds (*Tagetes* spp.) are amongst the most popular flowers and are ideal for garden display and loose flower purpose. High variability for both quantitative and qualitative character is available in this crop. Yield and its components are polygenic, hence are highly influenced by environmental factors. Therefore, it is essential to partition the over all variability in to its heritable over non-heritable components which will enhance the precision of selection. A detailed analysis of genetic parameters which will enhance the precision of selection. A detailed analysis of genetic parameters for nine quantitative characters in seven F_1 hybrids were studied, because reports on these aspects are inadequate to launch a productive breeding program. In the present investigation, it was observed that, variations were high for plant height, number of lateral branches per plant, number of flowers per plant and total yield per plant in the F_1 hybrids. In general, heritability estimates were high for all the characters except for number of lateral branches per plant, number of flowers per plant and total yield per plant. Among the characters studied. plant height, number of main branches per plant and total yield per plant had a high genotypic co-efficient of variation.

58

CHROMOSOME C-BANDING OF GENUS ANTHURIUM

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An established C-banding technique was modified to consistently yield complete set of distinct, sharply banded chromosomes in *Anthurium*. It was used to demonstrate similarities and differences among heterochromatin patterns of different species of *Anthurium*. The C-banding patterns showed a general agreement with heterochromatic knob positions known from pachytene studies. Two groups of banding patterns could be distinguished. Those species with bands that were almost exclusively terminally positioned included *A. andreanum* Lind., *A. scherizantum* Schott. and *A. crystallinum* Lind. In all, previously unknown heterochromatic regions were found. Both terminal and sub terminal band positions were found in *A. patulum* Lind. and *A. pentaphyllum* Lind. On the basis of these results, various breeding activities and taxonomic treatments of genus *Anthurium* and their closest relatives are questioned.

EFFECTS OF GAMMA RADIATION ON *IN-VITRO* PLANTLETS OF *DENDROBIUM* CV "SONIO" AND CV "KASIM WHITE"

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Two cultivars of *Dendrobium*, namely Cv "Sonia" and Cv "Kasim White" were propagated by *in-vitro* culture to provide numerous convenient plantlets. These were exposed to 0,5,10,15 or 30 GY of gamma rays to study their radio sensitivity, the dose rate was 2,5 GY/min. The plants of the C1 and C2 clonal generation showed decreases in plant survival rate, fresh weight gain and micro-propagation rate with increasing doses of gamma radiation. On the basis of survival, LD 50 was approximately 15 GY. The 30 GY dose drastically affects the different responses studied. It proved lethal on induced dwarf plants. Some plantlets, produced *in-vitro* from treated plants and showed morphological abnormalities of leaves or of whole plant. Further cytological studies revealed chromosomal abnormalities like laggards and stickiness. Above all, this technique has potential for increasing the genetic variation in *Dendrobium*.

GAMMA RAYS INDUCED BOLD SEEDED HIGH YIELDING MUTANT IN CHICKPEA (*CICER ARIETINUM* L)

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Induced mutation has played a significant role in the development of many crop varieties and is instrumental in enhancing genetic variability.

In the present work, dry and healthy seeds of chickpea (*Cicer arietinum* L.) Var. Pusa-212 were subjected to gamma irradiation and chemical treatments. The M_2 population was thoroughly screened for viable macro-mutations. A vigorous and bold seeded mutant with alterations for grain characters (grain shape and test weight) was identified in 40 KR gamma ray irradiated plant population. Almost all morphological parts of the mutant (leaf, petiole, flower, pod, seed etc.) were double in size than their respective parts in parental variety. Observations recorded on various quantitative traits in M_3 revealed a significant increase in yield per plant (g), plant height

and number of branches, whereas the number of pods per plant and number of seeds per pod decreased over control. The test weight (g) increased more than double as compared to control, but the seed protein did not show any appreciable change. The genetic parameters viz. PCV, GCV, h^2 and GA were quite high as compared to control. Cytological investigation of the mutant revealed perfect 8 bivalents ($2n=16$) at metaphase and did not show any major chromosomal abnormality.

61

CLASTOGENIC EFFECT OF CHEMICAL MUTAGENS IN *TRIGONELLA FOENUM-GRÆCUM* L

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Relative effects of Sodium azide (SA), Maleic hydrazide (MH) and Dimethyl sulphate (DMS) on meiosis and pollen sterility were studied in *Trigonella foenum-græcum* L. in M_1 generation. Meiotic studies revealed various aberrations like stickiness, laggards, univalents, multivalents, bridges, precocious separation, micronuclei, disturbed polarity and cytomixis etc. Stickiness of chromosomes, was the most common aberration followed by univalents and multivalents. Among the different stages of meiosis, the frequency of meiotic aberrations was maximum at metaphase stage. The frequency of meiotic aberrations and pollen sterility showed a linear increase with dose/concentration, with all the three mutagens. However, DMS induced maximum frequency of meiotic aberrations followed by MH and SA. Pollen sterility seems to be the cumulative result of various meiotic aberrations.

62

GENETIC AND POLLEN STUDIES IN *GLADIOLUS* spp

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Variability studies among 35 *Gladiolus* genotypes [11 Indian and 24 exotic] for 30 characters conducted at the Indian Institute of Horticultural Research, Hessaraghatta, Bangalore during 1998-99 revealed that, all the genotypes exhibited wide range of variation for days for spike emergence, floret size, number of florets open at one time, number of florets per spike,

spike length, rachis length and number of cormels per corm. For all the 30 characters studied, the differences between phenotypic and genotypic coefficients of variation were narrow indicating less environmental influence on their expression. High phenotypic and genotypic co-efficients of variations, heritability and genetic advance recorded for number of shoots per plant, number of spikes per corm, number of daughter corm, number of cormels per corm and 25 cormel weight suggests selection of genotypes based on these traits for further improvement through effective breeding programmes.

The most important hurdle a breeder encounters in *Gladiolus* breeding programmes is the asynchronous flowering of different cultivars. Pollen storage is one of the methods to overcome this problem. It also enhances the efficiency of breeding programmes by avoiding the cultivation of male parents. Pollen from five *Gladiolus grandiflorus* varieties viz. Darshan, Dhiraj, Sagar, Sapna and Shobha developed at I. I. H. R. and *G. calliantus* a wild fragrant species were stored at -65°C for three days and nine months and -196°C (in liquid nitrogen) for three days. The findings revealed negligible loss in the viability of pollen measured in terms of germination % *in vitro*, vigour (tube length) and fertility assessed through the number of seeds set per capsule upon pollination compared for fresh pollen. Since the above results also indicate no species/variety/duration specific pollen storage temperature, establishment of 'Pollen Banks' would assist *Gladiolus* breeders to overcome the problem of asynchronous flowering among the genotypes and would also aid exchange of germplasm.

Fusarium wilt is a major threat in the commercial cultivation of *Gladiolus* and is being controlled using fungicides. Development of resistant varieties is the best way to combat the disease problem for the present day eco-friendly environment. Screening of *Gladiolus* genotypes for *Fusarium* wilt resistance through conventional methods is time consuming, requires abundant plant populations, leads to the destruction of susceptible genotypes and the results may be some times inaccurate. Availability of pollen in abundance can be made use of for the above purpose. It also reduces the time required for screening apart from being accurate. A preliminary attempt was made to screen resistant (Dhiraj and Psittasinum hybrid) and susceptible (Friendship and Pricilla) genotypes for their resistance/susceptibility against *Fusarium* wilt through *in vitro* pollen studies. The results of the will be are discussed.

CENTELLA ASIATICA DETECTED AS BIOINDICATOR OF WATER AND SOIL POLLUTION

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Centella asiatica (Linn.), urban, a prostrate common herb of the family Apiaceae in cooler parts of North India was found to be a variable taxon in its morphological attributes and meiotic chromosomal characteristics in relation to its habitat. Found on the embankments of ponds, it showed definite pattern of irregularities during meiosis in relation to p11 and level of pollution of water. Irregularities included asynapsis desynapsis, multivalent formation, transmigration of chromatin between pollen mother cells, lagging of chromosomes at anaphases and complete failure of anaphasic segregation in different cases. Leaf growth and flower production were found to be directly related with the degree of meiotic irregularities. In heavily polluted conditions, plants were completely absent or extremely rare, found only in small niches, typified by relatively pure soil water content but *always* with highly reduced growth and minute leaves. Plants growing in coal deposited areas near railway tracks also showed morphological and meiotic aberrations but they were quite different in pattern from those found near polluted water bodies. Nevertheless, they were apparently the result of poor responses of the plant to the excessive carbon content in the habitat and lack of ideal moisture laden soil. All studies led to the specific assumption that the plant may be regarded as a very dependable bio-indicator of soil and water pollution.

EFFECT OF SOIL AND FOLIAR NUTRIENT APPLICATION ON BIOCHEMICAL COMPOSITION OF MULBERRY

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Mulberry leaf forms the sole source of food for silkworm (*Bombyx mori* L.). The protein content of mulberry leaf material is bio-synthesized into silk protein. Mulberry leaf plays a predominant role in the nutrition of silkworm and inturn cocoon production. The use of commercial nutrients is necessary to be used as soil application and liquid nutrients in mulberry cultivation,

as they are the mixtures of many primary and secondary nutrients. Multiplex is one of the commercial soil and foliar formulation stated to contain zinc, magnesium, copper, calcium, manganese, iron, boron, molybdenum, sulphur and nitrogen i.e., both macro and micronutrients. The experiment consists of three replications and four treatments with varying levels of multiplex micronutrient fertilizer as soil application (10kgs/acre) (T1), multiplex liquid spray (5ml/litre) (T2), zinc high (3g/litre) (T3) as foliar spray and the control plots were not treated T4. M-5 variety of mulberry was selected for the study. The plants treated with multiplex foliar nutrients (zinc high and liquid spray) showed a significantly high amount of proteins, soluble sugars and chlorophyll pigments viz., chl-'a', chl-'b' and total chlorophyll. The mineral constituents (micronutrients) were found significantly high in the leaves of mulberry plants treated with multiplex zinc high (T3) followed by multiplex liquid spray (T2) and multiplex soil application (T1). Multiplex micronutrient fertilizer has got all the secondary and micronutrients in balanced and easily available form for the healthy growth of mulberry which caters and complete nutritional requirement of silkworms.

65

ASSESSMENT OF THE GENOTOXIC POTENTIAL OF *PTERIDIUM AQUILINUM* EXTRACT USING *ALLIUM* TEST

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Pteridium aquilinum a common Pteridophyte of family Polypodiaceae is used by tribal for fuel, food and medicine. It is also used as compost and for washing the cloths because of its high potash content. It has wound healing and antihelmintic properties and also used in burnings and to kill both broad and long worms in the body. Biochemical investigation revealed that *Pteridium* contains insect moulting hormones like ecdysone and ecdysterone. The cynogenic glycosides (failed alkaloids) are found in considerable amount and these are toxic because they yield HCN when hydrolysed enzymatically. *Pteridium* found toxic and carcinogenic in mouse and cattle, hence the present investigation was planned to assess the genotoxic potential of *Pteridium aquilinum* extract using *Allium* test. Mature fronds were extracted in ethanol and the extractive dissolved in distilled water was used for the treatments. The results revealed that the extract has positive impact at lower concentrations but at higher concentrations various cytological abnormalities were observed. The abnormalities observed were bi-

nucleate cells, clumping, precocious movement, multiple bridges, laggards, fragments and stray chromosome. It was found that the mitotic index was higher at lower concentrations but gradually decreased with increase in concentration of extract.

66

COLCHICINE PRODUCTION IN VITRO

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Iphigenia stellata Blatt is an ephemeral, endemic and endangered plant of Western Ghats. Its seeds contain highest amount of (1.22-1.90%) colchicine. Callus cultures were established from the shoot apices on Murashige and Skoog's (1962) basal medium supplemented with 2,4- Dichlorophenoxy acetic acid (2-4mg / l) and kinetin (2-3 mg/l) or 6- Benzylamino purine (2-3 mg/l). Calli were nodular and yellowish in colour. After four weeks of incubation calli produced colchicine and other alkaloids which in turn leached out into the medium. Qualitative analysis of the leached out compounds revealed the presence of certain novel alkaloids along with colchicine. However, few naturally occurring alkaloids were not produced *in vitro*.

The quantity of colchicine produced was found to be dependent on the age of the callus. An effect of phosphate, sucrose and photoperiod on the quantity of colchicine production is discussed.

67

BIOPHYSICAL AND BIOCHEMICAL CHARACTERISATION OF EMS AND SA INDUCED MORPHOLOGICAL MUTANTS IN STRAWBERRY

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Strawberry is a temperate fruit crop and rates high on the list of preferred fruits in the world. It is a rich source of Vitamin C, anthocyanine and minerals like calcium, phosphorous and potassium. In the present investigation, attempts have been made to induce mutations in strawberry cv. Sweet Charlie for several desirable characters using different concentra-

tions of EMS and SA. Various morphological mutants have been identified and isolated from vM2 and vM3 generations. Induced mutations were found to affect growth pattern, leaf morphology, branching, time of flowering, fruit shape and yield in terms of fruit number and weight. These mutants were characterized for their biophysical parameters like photosynthesis (Pn) and stomatal conductance (Cs) and biochemical parameters like protein, phenols, chlorophyll and Nitrate reductase (NAR) activity. Some of the mutants like broad leaf, dark green, bobust and large fruit showed higher values for photosynthesis (Pn), protein, chlorophyll and NAR. It was also found that the mutants with higher photosynthetic rate (Pn), nitrate reductase (NAR) activity, protein, chlorophyll and phenols were found more productive with better reproductive sink ability.

68

STUDIES IN MEDICINAL PLANTS OF GANGETIC PLAINS OF BIHAR I. CAESALPINIA CRISTA L

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Meiotic analysis of pollen mother cells of ten different populations of *Caesalpinia crista* L. syn. *Caesalpinia bonducella* Flem did not show any difference in chromosome number and meiotic mechanism but sharp variations were observed in recombination index and pollen viability. Pollen sterility or existence of defective anthers seemed to cause condition of apparent male sterility in many flowers especially on lower part of the inflorescence while presence of defective stigma in upper flowers seemed to induce female sterility in them. This probably helped in cross pollination by ruby blue chrysid insect adapted perfectly for hypogynous nectar sucking.

69

EMS INDUCED CHROMOSOMAL ABERRATIONS IN TWO VARIETIES OF SWEET BASIL

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Ethylmethane sulfonate (EMS) has been used extensively for inducing useful mutations and to increase genetic variability by plant breeders. The present studies pertain to study the effect of this chemical mutagen on cytological behaviour of two varieties of *Ocimum basilicum* (sweet basil)

namely, var. *thyrsiflorum* and var. *pilosum*. Presoaked seeds of both varieties were subjected to treatment with 4.6×10^{-2} M EMS solution for 10h, 14h and 18h. EMS treated seeds were sown in the pots. The seeds treated with water served as control. Young flower buds were fixed in Carnoy's fixative and cytological preparations were made using standard procedure. Plants raised from EMS treated seeds as well as the control plants uniformly showed $2n=48$. In control plants, the meiosis was perfectly normal leading to normal tetrads and viable pollen grains. As far as mutagens treated plants are concerned meiosis was normal in majority of plants. In few plants of var. *thyrsiflorum* raised from mutagen treated seeds (14h, 18h) cytological abnormalities (5.56 to 8.89% PMC) like stickiness of chromosomes at metaphase – I, laggards at A-I, T-I and bridges at A-I, T-I, A-II and T-II were observed. Similarly, in one taxa of var. *pilosum* 26.15% of PMCs exhibited laggards and bridges during A-I and T-I stages. However, in both the varieties there was no significant reduction in the pollen fertility. Overall, except in the above plants. EMS treatment was not able to induce large scale cytological abnormalities in M_1 of both the varieties of sweet basil.

70

MUTAGENIC STUDIES IN ONION (*ALLIUM CEPA* L.) MACROMOLECULAR ANALYSIS

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Present investigation deals with the effect of gamma radiations and sodium azide, alone and in combination, in onion (*Allium cepa* L.). For macromolecular/ analysis, M2 leaves of onion var. N-2-4-1 were used. In this, proteins, phenols, sugars, starch , chlorophylls etc. were studied, while for enzymatic activity, peroxidase was studied. Overall studies revealed that combined treatments of gamma radiations and sodium azide were stimulatory than the single or alone treatments of mutagens.

71

BAMBOO'S –A NOBLE GRASS FOR BIOTECHNOLOGICAL IMPROVEMENT IN GROWTH RATE AND BIOMASS

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Bamboo is a multipurpose tree and botanically one of the very few tree species having C₄ type of photosynthesis. This gives scope for exploiting this plant to enhance its existing growth rate and bio mass even under limited conditions of growth. In this direction a study is under taken through Ashoka Trust for the Research in Ecology and Environment (ATREE). A survey is being under taken to find out the population of natural bamboos and artificially regenerated bamboos in the representative Districts of the State of Karnataka , India. Information is also recorded on the age of the culms, number of culms per bush, size, length, internal length, number of nodes per culm and other important parameters are recorded using appropriate sampling techniques. The existence of different species of Bamboo's in different areas is also recorded. Besides this, the consumption and harvest by artisans from towns to grass root level is surveyed for further analysis. Based on this, in addition to the natural regeneration (even after harvest), the possibility of enhancing the growth rate and biomass through various growth parameters and physiological attributes, particularly the presence of PEP carboxylase (responsible for C₄ photosynthesis) unique to this plant can be harnessed keeping in view the efficient enzymatic / biochemical properties of this super enzyme. The group of plants can be subjected or expected to higher levels of light intensity and higher temperatures for which the plants respond resulting in better growth and biomass. These treatments can be conveniently blended with the growth regulators in standardized concentrations and combinations. The C₄ enzyme present in this plant can be isolated and characterised through isozyme analysis for its use in genetic engineering applications through tissue culture methods.

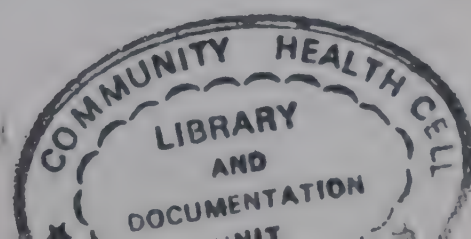
72

GENETIC VARIABILITY STUDIES IN HORSEGRAM (MACROTYLOMA UNIFLORUM (L.) VERDEC)

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Studies on genetic variability, heritability, heritability (broad sense) and genetic advance was carried out on 52 genotypes of horsegram during rabi season of 1997 at USA, Bangalore for 13 yield parameters. The results of the experiment revealed that GCV was less than PCV for all the traits which indicated that all the traits were highly influenced by environment. High PCV and GCV was observed for biomass, pod yield per plant followed by seed yield per plant, number of pods per plant and number of secondary



branches per plant. Comparatively narrow difference between GCV and PCV was observed for days to maturity, pod length, 100-seed weight and threshing percentage. High heritability coupled with high genetic advance was observed for biomass, pod yield per plant and seed yield per plant and high heritability coupled with moderate genetic advance was observed for plant height and number of primary branches per plant, suggesting that these characters can be considered for improvement through mass selection as they are more likely to be controlled by additive genes. High heritability coupled with low genetic advance was observed for days to maturity and 100 – seed weight, reflecting the operation of non-additive gene effects for these traits and selection for these characters will be ineffective.

73

EX-VITRO ESTABLISHMENT AND GROWTH OF HYBRID SEED-LINGS OF DENDROBIUM RELATION TO POTTING MEDIA

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In -vitro raised hybrid seedlings of *Dendrobium* required a period of humidity acclimatization in order to undergo morphological and physiological adaptations for successful *ex-vitro* establishment . An improvised structure made of iron frame and polythene covering with a loose -bricks -and sand flooring helped to maintain high humidity during hardening. Establishment and further growth depended on the choice of an ideal potting medium. Potting media tried were coconut husk (T1) , coconut fibre (T2), soilrite (T3) , broken tiles + soilrite in 2.2: 1 ratio (T4) and broken tiles +charcoal +tree fern root in 2. 2:1 ratio (T5) . Growth was assessed using six parameters viz. Plant height , number and length of roots and number, length and width of leaves. Potting mixtures T4 and T5 were found to favour maximum survival and well balanced growth of seedlings after six months. In these treatments, tiles and charcoal provide the necessary anchorage while soilrite / fern roots supply the required moisture and aeration to the roots. The emphasis is on an ideal balance between the supporting and supplying systems in the rooting medium whereby survival is maximised and growth is optimised.

CYTOLOGICAL STUDIES IN SOME MEMBERS OF GENTIANACEAE

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Karyomorphological, meiotic and cytotoaxonomic studies have been made in South Indian species of *Enicostema* (1 species), *Centarium* (1 species), *Hoppea* (2 species), and *Canscora* (7 species) of subtribe Erythrinae and tribe Gentianeae of the family. Altogether, 40 populations have been investigated. Chromosome numbers for *Hoppea* and *Canscora* have been determined for the first time. *Centarium* is found to have a chromosome number of $2n = 56$ with a basic number of $x = 7$ or 14 . Two species of *Hoppea* share a common chromosome number of $2n = 38$. *Enicostema* also has $2n = 38$ but one of the populations revealed a meiotic number of $n = 38$ indicating polyploidy in the genus. Out of the species of *Canscora* studies, three are diploids ($2n = 38$), two are tetraploids ($2n = 76$) and the other two species have both diploid ($2n = 38$) and tetraploid ($2n = 76$) populations indicating the possible role of polyploidy in speciation in this genus also. *Enicostema*, *Hoppea* and *Canscora* have the basic number of $x = 19$, which appears to be a secondary basic number. Meiosis was found to be normal in all the taxa studied. The somatic chromosomes are generally short with either median to subterminal centromeres and the karyotypes are generally short with either median to subterminal centromeres and the karyotypes are more often asymmetrical and seem to be of advanced nature. In *Centarium*, there is one pair of much longer chromosomes than the rest of the pairs, a feature also found in species from temperate regions.

CHARACTER ASSOCIATION AND PATH COEFFICIENT ANALYSIS IN F₂ GENERATION OF VEGETABLE COWPEA (*VIGNA UNGUICULATA* (L.) WALP)

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The knowledge of correlation helps in determining the relative importance of component characters influencing yield and path coefficient analysis provides an effective means of partitioning direct and indirect causes of

association. Correlation and path analysis thus help in identifying suitable selection criteria for improving yield. With this in view, about 140 F₂ plants were studied in the two crosses viz. Sel -11 x APC-729 and RCV-7 x APC -729 during the summer season of 1998 at the experimental field, UAS Hebbal , Bangalore and observations were recorded on 12 metric traits.

Phenotypic correlation coefficient of green pod yield with different components was estimated in the above crosses. Pod yield exhibited a high degree of significant positive association with number of pods per plant in cross Sel -11 x APC -729, whereas in the cross RCV -7 x APC 729 pod yield per plant exhibited a high degree of significant positive association with number of pods per plant, 100-green seed yield showed that green seed yield per plant exhibited maximum direct effect in both the crosses. Hence, selection for number of pods per plant, green seed yield per plant, plant height, number of secondary branches and 100-green seed weight would contribute greatly towards enhancing green pod yield in vegetable cowpea.

76

INTER-GENERATION CORRELATION AND NARROW SENSE HERITABILITY IN VEGETABLE COWPEA (*VIGNA UNGUICULATA* (L.) WALP)

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Inter generation correlation and narrow sense heritability, test the value of early generation selection. The interrelationship between yield and yield components in F₂ and F₃ generations of cowpea crosses was estimated with a view to identify characters and their combinations which might be useful as indicators of high yield. According to Miller *et.al.*, (1958) the correlations analysed and the interrelationships might be quite different in other materials in which gene associations exist in the parental lines of segregating population, or in which the mean values of the traits under study were different. Hence, correlation was computed for each of the four crosses viz., Arka garima x VS -389, Sel-11x VS -389, Sel -11xAPC-729 and RCV-7 x APC -729.

F₂ and F₃ generation of the above mentioned crosses were grown at the experimental field, UAS Hebbal, Bangalore during summer and kharif seasons of 1998 for F₂ and F₃ generations respectively and observations were recorded on 12 metric traits.

Inter generation correlation between F₂ and F₃ generation was non significant in all the four cross combinations studied. Narrow sense heritability was moderate for number of primary branches in cross RCV-7xAPC-729. Narrow sense heritability was quite low for all the other characters, suggesting non additive nature of gene action. Selection based on inter-generation correlation may not be effective in the above studied crosses in vegetable cowpea. However, selection for green pod yield per plant in early generations is worth attempting.

77

REACTION OF BITTER GOURD (*MOMORDICA CHARANTIA* L.) GENOTYPES OF DISTORTION MOSAIC VIRUS

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Bitter gourd is an important cucurbitaceous vegetable grown in different parts of India. Among various diseases affecting the crop, distortion mosaic disease has become a problem in Kerala recently, causing serious damage and thereby reducing the yield considerably. In the present study, 90 bitter gourd genotypes collected from different parts of the country were screened for their resistance reaction to bitter gourd distortion mosaic virus (BDMV) under natural condition. Crop was raised in the field with a spacing of 1.75 x 1.75m adopting all cultural and agronomic practices as per KAU package of practices recommendation, (Crops 1996). No plant protection measures were taken to avoid the destruction of vector population. The differential responses of genotypes of the BDMV were recorded and it was observed that out of 90 genotypes evaluated, 69 per cent of genotypes showed field tolerance to the disease. Disease symptoms started as mild mottling to severe distortion of the leaves, which spread rapidly throughout the plant. Among affected genotypes, 39 percent of genotypes showed symptoms before flowering, led to complete crop loss and 61 per cent of genotypes were affected after flowering which produced few, smaller and malformed fruits.

78

SCREENING OF CHILLI GERMPLASM FOR ANTHRACNOSE (*COLLETOTRICHUM CAPSICI*) RESISTANCE

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Screening of chilli genotypes of *Capsicum annuum*, *C. frutescens* and *C. chinense* against fruit rot and die back was undertaken to identify resistant to anthracnose. About 80 genotypes were screened under natural infection in the field. The percentage of disease incidence (PDI) was calculated with the help of Leaf spot, Die back and Ripe fruit rot. Changes in Bio-chemical constituents like Capsaicin content, Reducing sugars, Total sugars and Total Phenols of the fruits were also analyzed. Capsaicin content and Sugars were high in healthy fruits and Phenol content was high in diseased fruits. The highest GCV, PCV and heritability was obtained in the die back incident (78.2, 78.7 and 98.3% respectively). Capsaicin content was negatively correlated with die back and fruit rot (-0.418 and -0.474). Among the genotypes screened, 20 varieties (Pusa Sadabahar, Punjab Lal, Arka Lohit, CC 3, CC 4, etc) were found to be moderately resistant to the disease.

79

ASSOCIATION ANALYSIS IN CHILLI (*CAPSICUM ANNUUM* L.) GENOTYPES GROWN UNDER IRRIGATED AND RAINFED CONDITIONS

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Phenotypic and genotypic correlation co-efficients were estimated among nine characters in sixty genotypes of chilli grown under irrigated and rainfed conditions at Gandhi Krishi Vignana Kendra, Bangalore during 1993-94.

Plant height, spread of plant, total number of fruits per plant and fresh mean yield per plant had significant positive correlation with dry fruit yield per plant and dry per plant and dry fruit yield per hectare both under rainfed and irrigated conditions at phenotypic level. Days to 50 per cent flowering exhibited negative association with total number of fruits per plant, fresh mean yield per plant, dry fruit yield per plant and dry fruit yield per hectare under rainfed conditions at phenotypic level.

At genotypic level, plant height, number of branches per plant, spread of plant, total number of fruits per plant, final whole plant dry weight and fresh mean yield per plant showed significant positive association with dry fruit yield per plant and dry fruit yield per hectare under rainfed conditions.

Days to 50 per cent flowering manifested negative significant correlation with fresh mean yield per plant under irrigated conditions.

SEASONAL FLUCTUATION IN MEIOTIC BEHAVIOUR OF *SOLANUM TORVUM* SWARTZ

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Solanum torvum, Swartz. of Solanaceae prefers to grow in cool and shady habitat in the plains of north India and adjoining terai region of Nepal along with its immediate hilly tracts. Plants growing in hilly zones are not only luxurious in general growth but their microspore mother cells of the floral anthers showed perfect regular meiosis during whole flowering period which extends from cooler days of February to November through warm days of summer. Plants adapted to hotter plains were found to show varying response to seasons. Meiosis was normal in February - March but highly irregular during April-May while during October-November, sterility was encountered in most of the flowers. Such response to climate might be due to malfunction of genes responsible for meiotic process and pairing behaviour of chromosomes induced by higher temperature for which plant is not probably adapted properly. As almost normal fruit and seed setting was observed even during hot months, it is suspected that some kind of apomixis such as apospory or apogamy may be operative in the taxon which can only be revealed by suitable embryological investigations.

STUDIES ON THE POLYTENE CHROMOSOMES OF AN UNIDENTIFIED SPECIES OF *CHIRONOMUS* FROM JAMMU REGION

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A standard polytene chromosome map has been constructed for an unidentified species of *Chironomus*, designated here as *Chironomus* species II. The larval and pupal forms of this species were collected from a permanent water body in Farooq Nagar locality of Jammu region, J & K State, India.

The polytene chromosome complement of *Chironomus* species II comprises four chromosomes marked as I, II, III and IV which lie separate due to the absence of chromocentre. The seven chromosome arms have been designated a A-G following the scheme put forth by Keyl (1962). The nucleolar region is observed in the region 4C of chromosome I. The chromosome IV shows a very high degree of asynapsis. *Chironomus* Species II is found closely related to *Ch. plumosus* (Belyanina 1979); *Ch. Oppositus* (Martin 1969); and *Chironomus* species I (Sharma *et al.* 1990)

CHROMOSOMAL POLYMORPHISM IN TWO POPULATIONS OF *ANOPHELES STEPHENSI*

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The present study has been carried out on the chromosomal polymorphism in two populations of *Anopheles stephensi*, collected from the beds of river Tawi near Pir-Kho, Jammu (J&K) and from Nadasahib, Chandigarh. The polytene chromosome preparations have been made from the salivary glands of the fourth instar larvae following the technique of French *et.al.*(1962) with slight modifications. The chromosomal aberrations recorded include two inversions in Jammu population while three inversions and one translocation in Chandigarh population. A centromeric loop has also been observed in 2L of Chandigarh population. The inversions have been recorded in 2R, 3R and 3L, while the translocation observed in Chandigarh population involves zone 3 of X-chromosome and 31 of 3R.

KARYOMORPHOLOGY OF FOUR SPECIES OF SOUTH INDIAN SHORT-HORNED GRASSHOPPERS (FAM : ACRIDIDAE)

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Karyotypes of four species of short-horned grasshoppers, namely, *Leva indica*, *Dociostaurus species A*, *Catantops pinguis* and *Acrotylus humbertianus* from Dakshina Kannada region were prepared and studied employing conventional cytological and C-banding techniques. All the species studied exhibited $2n = 23$ in males and $2n = 24$ in females. Except one chromosome in *Leva indica* (metacentric) and one pair in *Dociostaurus species A* (submetacentric), all other chromosomes were found to be telocentric. The karyotypes for *Leva indica* and *Dociostaurus species A* are reported for the first time. The occurrence of metacentric and submetacentric chromosomes without the chromosome number being reduced, indicated the possibility of pericentric inversion during chromosome evolution. Details of chromosomal evolution are discussed.

IN VIVO RADIOPROTECTIVE EFFECT OF α - TMG AGAINST RADIATION INDUCED CHROMOSOME DAMAGE IN MOUSE BONE MARROW

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α -TMG, 2-(α -D-glucopyranosyl) methyl -2,5,7,8,- tetramethylchroman -6-ol, a water soluble derivative of vitamin E, has been shown to possess significant antioxidant activity *in vitro* (Murase et al. 1998) and to increase survival of lethally irradiated mice (unpublished). Part of the structure of TMG is similar to that of orientin, a plant flavonoid, which was found to have significant radioprotective effect *in vivo* (Uma Devi et al. 2000). Therefore, we studied the radioprotective effect of TMG on mouse bone marrow chromosomes after sublethal (1-5Gy) whole body gamma irradiation. Adult Swiss albino mice were injected intraperitoneally with 0.4 or 0.6g/kg TMG within 5 min of irradiation and 24h later the animals were sacrificed and their femur marrow were processed for chromosomal aberration study and micronuclei assay. Radiation produced a significant dose dependent in-

crease in the percent aberrant cells as well as the number of micronucleated polychromatic and normochromatic erythrocytes (MPCE and MNCE) and a significant decrease in the number of PCE. Post treatment with TMG (0.4 or 0.6g/kg) produced a significant reduction in the percent aberrant metaphases as well as the types of aberrations and in the number of MPCE and MNCE. TMG post treatment also increased the number of PCE compared to the irradiated control. TMG dose of 0.6g/kg provided the maximum protection without accompanying drug toxicity. TMG provides protection almost equal to the parent compound, vitamin E, but its high water solubility makes it a better candidate for protection against accidental exposure.

85

MOLECULAR CLONING AND CHARACTERIZATION OF β -ACTIN PROMOTER OF INDIAN MAJOR CARP, LABEO ROHITA

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The β -actin gene promoter from Indian major carp, rohu, *Labeo rohita* was isolated by Polymerase Chain Reaction (PCR) technique. Primers were designed from the sequences of other carps to amplify the β -actin promoter region. These primers amplified the expected length of 1.7kb fragment of the β -actin promoter region of rohu and catla. This 1.7kb fragment was cloned in a plasmid vector and partially sequenced. Molecular analysis of this sequence showed 93 and 92% homology with Grass carp (*Ctenopharyngodon idella*) and Common carp (*Cyprinus carpio*), respectively. Further analysis of the regulatory elements including the proximal promoter elements like TATA box and CAAT box and the evolutionarily conserved CC (A/T)₆ GG, (CArG or serum-response elements) sequences. There were two CArG motifs, one positioned in the promoter region between the CAAT and TATA boxes, and other in the first intron.

86

CLONING AND EXPRESSION OF GROWTH HORMONE cDNA OF CATFISH HETEROPNEUSTES FOSSILIS

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The Growth Hormone (GH) encoding cDNA has been isolated from the

pituitary cDNA library of *H.fossilis* and sequenced (Gen Bank Acc. No. AF 147792). The nucleotide sequence showed an open reading frame (ORF) of 600 bp, which was cloned into an *E. coli* expression vector and expressed under the T5 promoter. The full-length GH cDNA has been cloned into two eukaryotic expression vectors and the expression of the GH in Zebrafish has been confirmed.

87

ISOZYMES : A BIOCHEMICAL MARKER IN STUDY OF POPULATION GENETICS OF LABEO FIMBRIATUS (BLOCH.)

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Labeo fimbriatus (Bloch.) is an endangered species of peninsular Indian carp, therefore a study of its genetic diversity using isozymes as a biochemical marker was applied among two geographically distant populations. Ten enzyme systems standardised from the muscle tissue were used for this study viz, ALD, CAT, EST, EST-D, IDH, LDH, MDH, ME, PGI and PGM and isozyme was done using starch gel electrophoresis. Zymograms depicted no variation with respect to ten enzyme systems, indicating monomorphism of these enzyme loci, whereas these enzyme systems, are capable of distinguishing inter species differences among carps. Further studies are required with geographically distant and isolated populations of *Labeo fimbriatus* to confirm the existence of polymorphism and its further use as a chemotaxonomic marker.

88

ISOZYMES, PROTEIN MARKERS AND RAPD MARKERS USEFUL IN SPECIES IDENTIFICATION AMONG CARPS

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Species are the units to measure ecological diversity and alleles are the units of genetic diversity. Three different types of markers were used to study the interspecies variability among different species of carps viz, *Labeo fimbriatus*, Rohu, Catla, Mrigal, Tor, Common carp, Grass carp and Silver carp. Isozyme banding pattern of the ten enzymes showed species specific patterns. SDS-PAGE of sarcoplasmic protein profiles between species of

carp also showed a similar trend as isozyme data. RAPD analysis was done with 11 random decamer primers, 98.81% polymorphism was observed and could distinguish all eight species of carps with several unique RAPD bands. Our results emphasized that isozymes and protein profiles can be used in chemotaxonomic studies, where as RAPD could be used in population genetics, analysis of genetic diversity and conservation.

89

RANDOMLY AMPLIFIED POLYMORPHIC DNA (RAPD) MARKERS IN POPULATION GENETIC STUDIES OF *LABEO FIMBRIATUS* (BLOCH.)

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Randomly amplified polymorphic DNA (RAPD) analysis was applied to determine the genetic diversity among two geographically distant populations of *Labeo fimbriatus*. RAPD products were generated with eighteen 10-mer oligonucleotide primers and separated by Polyacrylamide gel electrophoresis (PAGE) and silver staining. There was less intra population variation but considerable genetic variation (35%) was observed between two populations of *Labeo fimbriatus* indicating the existence of considerable genetic diversity. Our results provided evidence that RAPD marker can be used to discriminate the *Labeo fimbriatus* populations and could be used for genetic linkage mapping. It is concluded that the RAPD method is one of the most time saving and least expensive non-invasive method for detection of genetic variation in fishes that could be used to conserve the endangered fish species.

90

GENETIC DIFFERENCES IN TWO *AEDES* SPECIES FROM MYSORE

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Bioassay studies were performed in order to assess the comparative susceptibility status of two dengue vectors of Mysore namely, *Aedes aegypti* and *Aedes albopictus*. The bioassay was carried out against four important synthetic pyrethroids, deltamethrin, permethrin, cypermethrin and

alphamethrin following the WHO procedure. Studies were also carried out to investigate the variations in α and β -esterase, isozyme patterns and in the activity of some target enzymes such α -esterase, β -esterase, glutathione-S-transferase (GST) and glucose -6-phosphate dehydrogenase (G6PD) by spectrophotometric analysis. Results have revealed differential susceptibility among the two species in terms of LC_{50} and LC_{90} values. Gel electrophoretic studies have shown differential banding pattern in the α and β -esterase isozymes. Variations in the activity of different enzymes analyzed have also been recorded. All the results were verified statistically and were found to be significant.

91

STUDIES ON THE *IN VIVO* GENOTOXICITY OF LEAD ACETATE IN MOUSE

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Lead is one of the most common metals known to humans since the early ages. It is used in many industrial processes and it is present in air, food, water, soil, dust and snow (WHO 1984). As a consequence of its persistence in the environment , exposure to this compound has become a major public health concern. Toxicity of lead and its salts has been extensively studied in different biological systems. But there are conflicting reports on the genotoxicity and carcinogenicity of lead. Hence, in our investigation we have made an attempt to study the genotoxicity of lead acetate in mouse system using different parameters like, Chromosomal aberration assay, Micronucleus assay, Sperm abnormality assay and Trans-placental micronucleus assay. In the present paper , results of our studies on the bone marrow micronucleus assay and sperm abnormality assay will be presented and discussed.

Three doses of lead acetate, viz 50mg, 100mg and 150mg/kg body weight were selected for our studies based on the LD 50 values already available. The chosen doses were less than LD 50 values. Each dose of the chemical was prepared in sterile distilled water and administered to experimental animals intraperitoneally. Bone marrow MN preparations were made at 24, 48, and 72 hours following the modified method of Schmid (1973) (Seetharam et al 1983). For sperm abnormality assay, above mentioned

doses of the chemical was administered once, and sperm preparations were made after 35 days to score different types of abnormal sperms, following the method of Wyrobek and Bruce (1975). The sperm count in the treated animals was also determined.

Lead acetate induced significant micronuclei at different doses and time interval. Scanning of slides of sperm abnormality is in progress. The results obtained for both of these tests will be discussed.

92

BIODIVERSITY OF *DROSOPHILA* SPECIES AT DIFFERENT SEASONS IN DEVARAYANA DURGA HILL KARNATAKA

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The genus *Drosophila* is very large comprising multitude of species distributed all over the world. Reference to literature has revealed that there are reports on the seasonality of *Drosophila* of Western ghats (Vasudev et al 2000, Prakash and Reddy 1979, Reddy 1973) but no information is available on seasonality of *Drosophila* from hills of plain region. Devarayana Durga is one such hill station situated across the eastern part of Tumkur District of Karnataka. This range of hills marks the boundary between Krishna and Cauvery river basins. The microclimatological conditions, narrow valleys, luxuriant flora and running streams with its moist surroundings, Devarayana Durga hills provide ideal abode for the colonization of several species of *Drosophila*. Hence, the present study is undertaken to understand the response of *Drosophila* to different seasons in this hill station. The results have revealed a total of 19 species belonging to two sub genera namely *Sophophora* and *Drosophila*. There is sudden richness of *Drosophila* populations in quantity and diversity during monsoon period. This is due to flowering and fruiting seasons with concomitant increase in decayig matter that provide ground for feeding and breeding. The effect of various environmental factors are different on different species as depicted in population peaks. The highest biodiversity in terms of number of species and highest quantity of flies are observed during monsoon period at an altitude of 820 mts. The results underline the importance of screening biodiversity of *Drosophila* in other parts of deciduous forest of interior Karnataka.

GENETIC VARIATION IN INBRED WHITE AND GOLDEN HAMSTER (*MESOCRICETUS AURATUS*)

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The Syrian (golden) hamster (*Mesocricetus auratus*) had become the third most commonly used laboratory animal in various research exceeded only by mice and rats. Thirty different mutations that have been developed since the introduction of the Syrian hamster as a laboratory animal in the 1930's, eighteen of these mutations involve coat and eye colour with the earliest being the brown cream, piebald and white hamster.

Inbred white (Syrian) hamsters, derived from golden hamsters (*Mesocricetus auratus*) in National Laboratory Animal centre, CDRI, Lucknow (India) were examined at 15 chromosomal loci coding body proteins and enzymes (Alb-I Akp-I, Car-1, Ce-2, C-3, ES-I, ES-2, ES-3, Gpi-I, Hbb, Idh-I, Mod-I, Pep-3, Pgm-I, and Trf-1) in cellulose acetate electrophoresis and compared the allelic patterns with inbred golden hamsters to establish genetic profiles, as well as genetic variation in between two strains. It has been observed that the Akp-I and ES-3 were different in white hamster, whereas other markers were similar in both strains. Three alleles (ABC) were found in Akp-I in both strains, but 'A' was dimeric (double banded) in golden hamster. ES-3 was two alleles (AB) in both strains but 'A' was trimeric (triple banded) in golden hamster and dimeric in white hamster.

It may be concluded that, white hamster derived after the mutation in golden hamster possesses marked difference in Akp-1 and ES -3, hence this pure inbred line of white hamster can be designated as a pure substrain of golden hamster.

BREEDING SYSTEM OF MANGOLIAN GERBIL (*MERIONES UNGUICULATUS*) IN RELATION TO BIOCHEMICAL MARKER STUDIES

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Mangolian Gerbil (*Meriones unguiculatus*) is used in large scale in

different biomedical research. Hence, the adoption of proper breeding system is essentially required for animal breeder to supply animals to the user and to maintain breeding colony ; but without genetic monitoring of breeding colony, it is not possible to adopt breeding system (Monogamus, Trio and harem breeding system) for a particular laboratory strains for their good propagation. Mangolian Gerbils are known as monogamus breeder, since 1980. The National Laboratory Animal Centre, CDRI, Lucknow has adopted monogamus breeding system to maintain the gerbil colony as the result of CI was very low (0.32) in 1997-1999. Therefore, the gerbils were examined at 15 chromosomal loci coding body proteins and enzymes (Alb-I, Akp-I, Car-I, Ce-2, C-3, Es-I, Es-2, Es-3, Gpi-I, Hbb, Idh-I, Mod-I, Pep-3, Pgm-I and Trf-I using cellulose acetate electrophoresis to know the allelic patterns of the outbred gerbil colony and to establish proper breeding system of this strain. It has been found that there was no polymorphism against 15 biochemical markers of the above outbred strains. In the outbred breeding system, heterozygosity within the strain is essentially required for proper production. Hence, we have adopted trio (2:1) breeding system instead of Momogamus pairing that enhanced high colony index (CI 0.93).

95

CHROMOSOME STUDY IN NINE SPECIES BELONGING TO FOUR MAJOR SUBFAMILIES VIZ. GALERUCINAE, CROCERINAE, CASSIDINAE AND EUMOLPINAE OF FAMILY CHRYSOMELIDAE

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The present investigation pertain to nine species of family Chrysomelidae viz *Kanarella* sp. I, *Kanarella* sp. II, *Galerucida rutilans* Hope., *Aulacophora intermedia* Jac., *Lema bohemani* Clark., *Lacoptera quadrimaculata* Thunb., *Lacoptera quadrimaculata* Thunb., (sub. Sp), *Aspidomorpha miliaris* Fabr., *Colasposoma ornatum* Jac. Of the four species belonging to sub-family Galerucinae, 3 have been worked out for the cytology. In one species, *Kanarella* sp. I, polyploidy could be observed. *Lema bohemani* with Xyp sex mechanism has been added to the cytology of Criocerinae. Three species of sub family cassidinae have been worked out during present investigations. Of which, one with XY male sex chromosome system is an addition to this sub-family. A progressive step wise increase in chromosome number by 2 could be observed, while working on *Colasposoma ornatum* by reporting chromosome number – 9 in sub family Eumolpinae for the first time. The

detailed features of chromosomes and the status of these 9 species will be elucidated.

96

PROTECTIVE EFFECTS OF ASCORBIC ACID AND PHYLLANTHUS EMBLICA AGAINST LEAD GENOTOXICITY IN GERM CELLS OF MICE

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Metals like lead constitute important class of toxic substances with potential health hazard. Among heavy metals, lead, is known mutagen in variety of test systems ranging from bacteria to mammalian cell culture is well documented (Kalyana Swamy et al 1993 and Foster et al 1996). Since past two decades global concern about the toxic effect of such metals particularly through environmental and occupational exposure is steadily increasing due to its long term consequences on public health. It is difficult to eliminate mutagenic factors present in our environment. Attempts have been directed for a better habits to protect against mutagens.

Ascorbic acid due to its reducing and chelating action exerts a wide variety of effects including antimutagenic and anticlastogenic properties (Mirvish 1975, Parshad et al. 1978, Gebhardt et al. 1985, Giri and Banerjee 1986). It has been shown to antagonise the toxic activity of certain metallic salts in mammalian system as well (Chakrabarty et al. 1977).

In the present investigation, the protective effect of synthetic Ascorbic acid (Vitamin-C) and *Phyllanthus emblica* evaluated against clastogenicity induced by lead nitrate (10,20 & 40 mg/kg) on the incidence of chromosomal aberrations and sperm head abnormalities was observed. It can be suggested from the above study that ascorbic acid (Vitamin-C) and *Phyllanthus emblica* to play a key role in inhibition of heavy metal mutagenesis in mammals.

97

CHANGES IN THE NUMBER OF SPERMATOGONIA AS A SIGN OF TESTICULAR DEGENERATION IN MICE

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Adult mice were administered six oral doses of malathion dissolved in corn oil per day-1 ppm, 10ppm, 100ppm, 200ppm, 400ppm and 800 ppm. The malathion treated, oil treated control and untreated control animals were sacrificed upon 10, 20, 30, 40, 50 and 60 days. The pieces of testes were fixed for histopathological examination. The number of spermatogonia per vision field was taken as a parameter to see the effect of malathion on testicular degeneration in mice.

The lower doses of malathion did not cause any significant change in the number of testes of mice. But at higher doses i.e. 400 ppm and particularly 800ppm had undergone a significant decrease which was a sign of testicular degeneration.

✓ 98

PERICENTRIC INVERSION POLYMORPHISM IN *GASTRIMARGUS AFRICANUS ORIENTALIS* (ACRIDIDAE)

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The karyotype is a basic feature of a species. Acridids are well known for their karyotypic uniformity in having exclusively acrocentric chromosomes in majority of species. The metacentrics have to be formed either by centric fusion or by pericentric inversion. The karyotype of *G. a. orientalis* has $2n=23$ in males and $2n=24$ in females. The karyotype includes three pairs of long, six pairs of medium and two pairs of small chromosomes. All the chromosomes are exclusively acrocentric except the 6th, 7th, 9th, 10th and 11th pairs of autosomes which showed structural variations. The 6th, 7th, 10th and 11th pairs exist as either acrocentric or metacentric chromosomes while the 9th pair of chromosomes are seen as submetacentrics or metacentrics. In all these individuals of *G. a. orientalis*, though there exists polymorphism for five pairs of chromosomes, the diploid number remains the same, being $2n=23$. Therefore, these metacentric chromosomes and its allies, must be the products of different pericentric inversions, which have altered the location of centromere. Implications of pericentric inversion polymorphism in the genome of an Acridid will be discussed.

LOCALIZATION AND CHARACTERIZATION OF HETEROCHROMATIN IN FOUR SPECIES OF THE MONTIUM SUBGROUP OF DROSOPHILA

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The karyotype is an important biological attribute of a species. It provides individuality and a cytotaxonomic status to a species. The study of karyotypic differentiation among taxonomically closely related species provides an insight into the still intriguing problem of chromosomal change during evolutionary process.

The *montium* subgroup is an important assemblage of the *melanogaster* species group of *Drosophila*. The wide geographical distribution, together with the wealth of species diversification within subgroup made the *montium* subgroup an attractive system for evolutionary studies. Of the 82 known species of the *montium*, about 50 species are known karyotypically and of these, the heterochromatin of only a few species has been characterized. Present study is undertaken with an intention to understand the metaphase karyotype differentiation among four species of the *montium* subgroup namely *D. agumbensis*, *D. anomelani*, *D. truncata* and *D. cauverii*.

Mitotic metaphase chromosomes of the neural ganglion cells were examined to know the chromosome number, the form and nature of the metaphase components. The C- and Q- banding techniques were applied to localize, to characterize and to quantify the constitutive heterochromatin in the metaphase karyotypes and inter-species comparisons were made pertaining to the chromosome constitution and heterochromatin distribution. These morphologically differentiated but taxonomically related species under study have shown remarkable differences in the pattern and the intensity of C- and Q-band heterochromatin, in general and Y-chromosomes and 4th chromosomes in particular. Implications of these findings will be discussed.

INSECTICIDE INDUCED ALTERATIONS IN THE MONOAMINERGIC SYSTEM OF DEVELOPING RAT PUPS

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Methyl parathion induced alterations in the level of monoamines viz., Norepinephrine, Dopamine and serotonin were studied in discrete regions of developing central nervous system of rat pups. A significant decrease in the level of monoamines noticed on methyl parathion toxicity may point to the altered neuronal activity and inefficiency leading to depression and impairment in various behavioural activities. In contrast to AchE inhibition in insecticide exposed animals, monoamine oxidase (MAO) activity has shown an increasing trend and may be found to cause deamination of catecholamines and accumulation of its metabolites. This leads to an inference, that an increased AchE inhibition indirectly stimulates MAO activity in developing rat pups exposed to methyl parathion.

101

PESTICIDE INDUCED CHANGES IN MEMBRANE LIPID PEROXIDATION IN DEVELOPING CENTRAL NERVOUS SYSTEM OF RATS

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Sub lethal doses of methyl parathion (o-o-dimethyl-o-nitrophenyl thiophosphate) injected intra peritoneally to developing rat pups induced alterations in the lipid peroxidative system. A significant increase in the rate of Malondialdehyde formation and a decrease in the levels of Sulphydryl groups, Glutathione and Catalase activity observed in the discrete regions of developing central nervous system indicates the peroxidative damages consequent to methyl parathion toxicosis. The data highlight the oxidative stress caused by toxic methyl parathion and anti oxidant mechanisms in the neurotoxicity.

102

PREVALENCE OF SIBLING SPECIES OF ANOPHELES CULICIFACIES GILES IN KARNATAKA

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Most of the malaria vectors exhibit species complexes. Generally members of complexes are morphologically similar, reproductively isolated

and show variations in their genetic structure. *An. culicifacies* is the principal vector of malaria in rural areas and is responsible for 60-70 % of total malaria in India. This species has a complex of five sibling species viz., A, B, C, D and E mainly differentiated on the basis of inversion polymorphism in polytene chromosomes of ovarian nurse cells. Among these sibling species, biological variations such as breeding site preference, resting and feeding behaviour, susceptibility to insecticides, vectorial potential are reported (Subbarao *et al.* 1999). In the recent years cross sectional and longitudinal studies on the prevalence of sibling species of *An. culicifacies* in different parts of Karnataka have been carried out. Cross sectional studies in the northern Districts Raichur, Gulbarga, Bijapur showed that species A, B and C are prevalent at 84.2%, 87.5% and 7.3% respectively ; while in southern Districts Mandya and Tumkur only species A and B were present at 78.2 and 21.8% respectively. Longitudinal studies carried out at Hassan and Kolar Districts reveal that species A and B were present at 67% and 32.2% respectively. In the peri-urban area near Bangalore City (village – Hosur Bande) both species A and B showed sympatricity at 49.4 and 50.6% respectively. Stratification of geographical areas based on sibling species complexes of vector mosquitoes would play an important role in the control of malaria.

103

CHROMOSOMAL CHARACTERISTICS OF AN OLIGOCHAETE *EUDRILUS EUGENIAE*

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Eudrilus eugeniae, an exotic earthworm, has been considered a serious contender of biodegradable activities in the soil resulting in a good quality vermicompost. A steady increase in populations and their capacity to organic waste recycling by voracious feeding habitation led us to take up a detailed analysis of chromosome biology of these earthworms.

Mitotic (using whole tissues of freshly emerged hatchlings) and meiotic chromosomes (derived from gonadal tissues of embryos and / or adults procured at appropriate time of development) were prepared by means of conventional air drying techniques and followed by the use of variable differential staining protocols on these preparations depending on the

purposes of the study (for example, to delineate chromosome dynamics). The somatic karyotype revealed a diploid number of 30. The pachytene karyotypes prepared from male and female cells and their comparison of individual bivalents showed their homological in a general way. Mitoses can be obtained from spermatogonial and in a few cases from blastomere divisions. In a nonspecific manner, some nuclei of blastomeres, provide a good number of polyploid complements.

In the light of the available chromosomal data, it is possible to imply that this species exists as a sexual diploid, and chiasmatic, with the notion that the haploid number of 15 could serve as basic ancestral number.

104

MEIOTIC CHROMOSOMAL ANALYSIS OF SOME SPECIES OF COLEOPTERA (SCARABAEIDAE) FROM SOUTH INDIA

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Meiotic chromosomal analysis was carried out in seven species of dung beetles belonging to the subfamily Coprinae viz. *Onthophagus dama* (F.), *O. recticornutus* Lansb, *O. igneus* (Vigors), *Oniticellus cinctus* (F.), *Onitis philemon* F, *Copris repertus* (Walk) and *Liatongus rhadamitus* (F.). Chromosomes were prepared following the air drying technique and the same were stained with conventional Giemsa (2%) solution. Diploid chromosome number in the surveyed species was found to be 20, Xyp and Xyr types of sex determining mechanisms were noticed which is typical for Scarabaeids. Karyotypic details and behaviour of chromosomes during male meiosis are discussed in this paper.

105

KARYOSYSTEMATICS OF INDIAN MIDGE *NILODORUM BIROI* (DIPTERA : CHIRONOMIDAE)

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The purpose of the present investigation was to describe and characterise the two cytological types of *Nilodorum biroi* (K) (the species belonging to *pseudothummi* group) a common midge found in south Indian regions.

Mitotic, meiotic and polytene chromosomal analysis revealed the existence of two readily recognisable chromosome types : one with four polytene elements ($2n=8$) and the other with only three ($2n=6$). In which G chromosome (N-end) was found tandemly fused with chromosome 3.

The present paper deals with the cytological characteristics to differentiate between the chromosomal forms and to indicate the relationship to each other based on several differential staining profiles (C-, NOR etc.).

106

IMMUNE RESPONSE OF VECTOR MOSQUITO *ANOPHELES STEPHENSI* TO MALARIA PARASITE *PLASMODIUM YOELII*

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Immune responses of the malaria vector mosquito *Anopheles stephensi* was monitored locally (Salivary glands and Midgut) and systemically (Haemolymph and Ovaries) by the induced expression of polypeptides after infection challenge, by the malaria parasite, *Plasmodium yoelii*. About 6 polypeptides were induced commonly in the four tissue examined. In addition, 15 polypeptides in salivary glands and 17 in midgut were induced locally and 15 systemically in the haemolymph and 14 in ovaries. Quantitatively, the amount of soluble proteins in oocysts and sporozoite positive mosquitoes was always less in the four tissues examined as compared to their normal counterparts. In the midgut, a robust response occurs between 24-36 hours post-infection, at a time when ookinetes traverse the midgut epithelium, but subsides. In contrast, the salivary glands show no significant response during this phase, but are activated in prolonged late phase when sporozoites are released from the midgut into the haemolymph and invade the glands between 16-24 days after blood feeding. The parasite evidently elicits immune responses in multiple tissues of the mosquito, two of which are epithelia so that parasite must traverse to complete its development. The observation that *Plasmodium* can trigger a molecularly defined immune response in a vector constitutes an important advance in our understanding of parasite -vector interactions that are potentially involved in malaria transmission, and extends knowledge of the innate immune system of insects of encompass responses to protozoan parasites.

107

ANTI-MOSQUITO OVARY ANTIBODIES REDUCE THE FECUNDITY OF *ANOPHELES STEPHENSI* (DIPTERA : INSECTA)

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Mosquito antigens that are normally not introduced into vertebrate host, when mosquito feeds can induce an artificial immune response. In the present study, it has been demonstrated that mosquito ovary immunogens induce the production of anti-mosquito ovary antibodies that reduce the fecundity and also the viability of progeny of *A. stephensi* which obtained blood meal of immunized rabbit. Rabbit antibodies to five antigens (AJ 29, 35, 43, 64 & 80 kDs) derived from the ovaries of *Anopheles stephensi* tended to reduce number of eggs produced. Ingestion of anti-mosquito ovary antibodies did not show detectable affect on mortality of mosquitoes. The antibody titer in the rabbit measured by ELISA against immunizing mosquito tissue antigen was also very high. Antisera raised against *Anopheles stephensi* ovaries were also used to identify cross-reactive immunogen in other tissues and in ovary of other species of *Anopheles* by western blotting. Results provide enough evidence for potential of anti-mosquito ovary antibodies to disrupt the reproductive physiology of mosquitoes and indicated need for further studies with target antigens.

108

ANTIMUTAGENIC STUDIES OF *ANONA SQUAMOSA* IN SOMATIC CELLS OF MICE

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Antimutagenic agents are natural or synthetic compounds which are able to lower or abolish genotoxic effects of mutagenic and carcinogenic factors by diverse modes of action. The search for antimutagenic agents is very important since mutagenic and carcinogenic factors are omnipresent in human environment and elimination of all of them seems to be impossible. In the present investigation, antimutagenic studies of seed extracts of *Anona squamosa* has been evaluated against cyclophosphamide in somatic cells of mice using the micronucleus assays in bone marrow and peripheral blood erythrocytes.

The animals were treated orally with 10% and 15% of the seed extract of *A. squamosa* for different durations (individual treatments) followed by cyclophosphamide for 24 hours (in combinations). The slide preparations were made according to the standard methods.

The results obtained in the present study showed the antimutagenic nature of *A. squamosa* in somatic cells of mice.

109

KARYOTYPE ANALYSIS OF THE INDIAN MAJOR CARP, LABEO BATA (CYPRIMIDEA, PISCES)

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The karyotype of an Indian major carp, *Labeo bata* from Satluj-Yamuna Link Canal (Haryana) was analyzed by using conventional Giemsa staining, Ag-NOR staining, C-banding and G-banding. The diploid chromosome number was found to be 50. The karyotype comprised 5 pairs of metacentric, 6 pairs of sub-metacentric, 6 pairs of subtelocentric and 8 pairs of acrocentric chromosomes. Distinct centromeric C-bands could be observed in some pairs, while others were almost uniformly stained. The amount of C-heterochromatin was observed to be much less in this fish as compared to other species. Densely stained homomorphic NORs were found localised on the terminal region of short arms of a subtelocentric pair. The prometaphase chromosomes of this fish could reveal positive G-bands by ASG method, thus facilitating the identification of homologous chromosomes. The present results indicate that some fishes might have chromosomes which respond positively to the G-banding and other structural banding, and that fishes may differ widely in their chromosome organisation so far as the response to banding is concerned.

✓**110**

GENOMIC ANALYSIS OF POLYTENE CHROMOSOME 2L (3) IN FIVE SPECIES OF THE GENUS ANOPHELES (CULICIDAE : DIPTERA)

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The limitations in the use of metaphase karyotype uniformity in number and morphometric variations and the applications of molecular taxonomy have greatly enhanced the importance of polytene chromosome banding pattern studies in mosquitoes. The puffing activity in these chromosomes also provides visual details of the biosynthetic activity of specific loci involved in intense local synthesis of RNA. The present paper deals with the genomic analysis of the left arm (2L) of chromosome 2 in five species of the genus *Anopheles* viz. *An. subpictus*, *An. willmori*, *An. maculatus*, *An. culicifacies* and *An. splendidus*. 2L is the shortest element representing the short arm of the submetacentric chromosome 2. It measures about 120-130 μ m in the first four species and 110-120 μ m in the remaining one. Out of a total of 650-700 recognisable bands in the entire set of three polytenic elements, 2L shares an average of 120 to 130 heterochromatic bands and 20 to 25 puffs, out of which 3 to 4 acquire Balbiani ring configurations at any given time in the life of fourth instar larva. As per the microdensitometric analysis, this chromosome carries about 20% of the total genomic content. As for the incidence of inversion polymorphism, it is fairly conservative to change next only to the X-chromosome. The present genetic documentation of 2L in the five species of the subgenus *Cellia* has been discussed in greater detail listing many other chromosomal markers of karyological interest.

111

GENETIC AND BIOCHEMICAL BASIS OF DELTAMETHRIN RESISTANCE IN *CULEX PIPIENS QUINQUEFASCIATUS*-A FILARIA VECTOR

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Culex p quinquefasciatus – the filarial vector is a very common species found in urban areas. The constant use of insecticides has led to the development of resistance in this species to various groups of insecticides including synthetic pyrethroids well known for their high knock down effect. In the present study, the genetic and biochemical basis of insecticide resistance to the synthetic pyrethroid deltamethrin and its effect on the biology of the mosquito was carried out. A homozygous resistant stock for 0.0035 ppm of deltamethrin 17 times higher than the LC50 value was established and the corresponding susceptible stock was isolated and purified. The data obtained from the various genetic crosses between the

resistant and susceptible individuals and their LC50 values revealed the degree of dominance as 1 indicating complete dominance. The same homozygous resistant stock of *C.p. quinquefasciatus* for 0.0035 ppm was subjected to quantitative analysis and PAGE for determining the electrophoretic pattern of proteins, enzymes-acid phosphatase, alkaline phosphatase, acetylcholine esterase, lactate dehydrogenase and glutathione-S-transferase. The difference in the electrophoretic patterns, zymograms and their relative mobilities between the resistant and susceptible stocks at the developmental stages of egg larvae, pupae and adults for deltamethrin in *C.p. quinquefasciatus* showed an marked increase in the resistant individuals than the susceptible individuals.

112

GENETICAL AND BIOCHEMICAL STUDIES OF FENITROTHION RESISTANCE IN *ANOPHELES STEPHENSI* LISTON

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Genetical and biochemical studies of Fenitrothion resistance were carried out in *Anopheles stephensi* Liston, the principal malaria vector in India. Fifteen strains of this species collected from different geographical areas were used to establish the baseline susceptibility status of this OP compound. The LC₅₀ in all the strains varied between 0.0023 and 0.004 ppm while LC₉₀ between 0.0045 and 0.01 ppm. The genetic mode of resistance was studied using a diagnostic dosage of 0.125 ppm to late third instar larvae of *Anopheles stephensi* in various genetic crosses which include homozygous fenitrothion resistant (*FNr*) and susceptible (*FNs*), F₁ hybrids, back crosses and F₂ generations. The data of genetic crosses between resistant and susceptible individuals revealed that the gene *FNr* is incomplete dominant and autosomal as the resistance was shown in both sexes for both F₁ hybrids and back crosses. The log -dosage probit lines for resistant and susceptible, F₁ and F₂ hybrids clearly showed the characteristics imparted by a single incomplete dominant gene. A remarkable variation on the reproductive potential and longevity of life cycle was also observed. Biochemical analysis of Polyacrylamide Gel Electrophoresis for protein and esterase isozyme patterns during the developmental stages (egg, larvae, pupae and adults) were carried out. The zymogram and relative mobility showed variation in the number and intensity of protein and esterase bands in the resistant strains as compared to the susceptible one.

This study would be of great help for proper and timely use of insecticides in the vector control programme.

113

GENETIC STUDIES OF "RUBY EYE" – A NEW EYE COLOUR MUTANT IN THE MALARIA MOSQUITO *ANOPHELES STEPHENSI* LISTON

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Anopheles stephensi Liston is an important malarial vector in the Indian subcontinent and middle-east. The chemical control is the chief method employed to control malaria in India. The chemical control, despite having the advantage of simplicity and convenience, has drawbacks such as development of resistance among vectors and environment pollution. Therefore, alternative strategies should be developed which does not involve resistance among vectors. Genetic control is one such method which does not involve resistant among vectors. Genetic studies of mosquitoes especially of species and strains which are vectors continue to be an essential component of genetic control strategies aimed at disrupting the transmission of diseases.

The present paper describes the isolation, establishment and genetic studies of spontaneously occurring eye colour mutant, ruby eye (*ru*) in *An. stephensi*. The mutant was isolated from the laboratory maintained strain of *An. stephensi*, which was originally collected from Poona , India. The ruby eye colour appears in the I instar larva and becomes very conspicuous in the pupae and freely emerged adults. Reciprocal crosses were made between the mutant and the wild type to establish the mode of inheritance of ruby eye. The data on the mechanism of inheritance of ruby eye clearly showed that gene "*ru*" is an autosomal and recessive with full penetrance and uniform expression in both sexes. The mutant is vigorous, requiring no more care than the wild type. This mutant can be used in applied genetic research, involving the synthesis of transgenic strains of *An. stephensi* for the genetic control programme.

GENETIC STUDY OF CYPERMETHRIN RESISTANCE IN THE MALARIA MOSQUITO , *ANOPHELES STEPENSI* LISTON

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Anopheles stephensi Liston , is an important vector of urban malaria in the Indian sub-continent. It is a member of the sub genus *cellia* and series *Neocellia*. A discriminating dose of 0.008 ppm Cypermethrin (RS)- L -Cyano - 3-phenoxybenzyl (I RS) - *cis* - *trans* - 3 -(2,2 - dichlorovinyl) -2,2 -dimethyl cyclopropanes carboxylate, a synthetic pyrethroid was used to separate the homozygous resistant (Cr) and susceptible (Cs) stocks of *An.stephensi* by selectively inbreeding for 24 and 6 generations respectively. The resistance/susceptibility tests were conducted in accordance with WHO (1981) procedure, using late third instar larvae. The larvae were treated with the diagnostic dosage for 24 hours after which mortality (susceptibility) and survivability (resistance) were recorded. The diagnostic dosage of 0.008 ppm for cypermethrin was fixed according to the procedure of WHO (1981). Mendelian crosses were carried out between the resistant and susceptible individuals and the individuals obtained after each genetic cross were subjected to insecticide treatment with the diagnostic dose and the LC₅₀ values were calculated. They were scored for mortality/resistance after 24 hours with sex ratio also being taken into consideration. The Chi square values were calculated. The relationship between dosage and mortality of cypermethrin resistance and susceptible strains were established for third instar larvae for the different genetic crosses. The Log-dosage-probit (LD-P) lines were constructed for each of the crosses. The LD-P lines of resistant and susceptible stocks and F1 and F2 progeny indicated that the gene *Cr* is a single incompletely dominant and autosomal gene.

KARYOTYPIC STUDIES ON SIX SPECIES OF PASSERIFORMES

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Diploid number of chromosomes in six species of birds (Aves : Passeriformes) belonging to there families have been investigated. These are : *Lanius schach* (Vigors) (Laxiidae) *Pericrocotus cinnamomeus* (L)

(Campephagidae), each with $2n = +72$; four species of *Muscicapidae* viz *Muscicapa thalassina* Swainson $2n = +70$, *Orthotomus sutorius* (Latham) $2n = +72$. All the species possessed ZZ:ZW sex chromosome system. The karyotypes comprising macro - and micro-chromosomes have been described. Evolution of karyotypes and phylogenetic interrelationships in Passeriformes have been discussed.

116

PERFORMANCE STATISTICS OF FRIESWAL COWS

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Project Directorate on Cattle (ICAR), Meerut has been engaged in evolving a new breed of cattle 'Frieswal', a Holstein -Sahiwal crossbred, with the collaboration of Directorate of Military Farms. Data recorded from 27 military farms over a period of eight years from 1990 to 1997 were analyzed to study the production performances (yield in 300 days or less : 300 DY, total lactation yield: TLY, lactation length : LL and peak yield : PY) of Frieswal cows. A total of 2435 lactation records were utilised for this purpose. Another set of data comprising 1123 first lactation records from 15 military farms were analysed for age at first calving (AFC) of Frieswal cows. A third set of data comprising 1632 records from 27 military farms were utilized for studying the reproduction traits (dry period : DP, service period: SP and calving interval: CI) of Frieswals. Each year was divided into three seasons, viz . winter (Nov. to Feb.) , summer (March to June) and rainy (July to Oct.).

Least squares analysis of variance technique using Harvey's software (1990) was applied to analyse the data. The overall herd averages of AFC, 300 DY, TLY, LL and PY were 993.7 ± 10.4 days, 3211.4 ± 117.2 kg, 3555.4 ± 154.1 kg, 357.7 ± 12.6 days and 14.9 ± 0.6 kg respectively. The reproductive statistics including DP, SP and CI averaged 153.2 ± 15.2 days, 230.1 ± 22.4 days and 513.5 ± 21.8 days respectively.

It was observed that in AFC and all the production traits, farm, year and season effects were highly significant. Lactation order was highly significant for most of the production traits except the lactation length where the lactation order had no significant effect on this variable.

However, in reproduction traits, the year effect reflecting mainly the managemental variability over the years were significant. The farm and lactation (parity) effects were highly significant for all the reproductive traits which were expected also due to variations in farm management and lactation length in different lactations. Year and season had significant effects on SP and CI, but didn't have any significant effects on DP. The performance statistics of Frieswal cows showing the production and reproduction traits were well within the expected values and not much varying at the 27 different farms.

117

MECHANISM OF DEATH SIGNAL TRANSDUCTION PATHWAY INDUCED BY BUTYRIC ACID IN VIVO

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Dietary fibre (DF) is known to prevent cancer of the lower bowel. Short chain fatty acids (SCFA) are the end products of fermentation of DF by intestinal microflora. The SCFA produced are acetic acid, propionic acid and butyric acid (BuA). BuA is a four carbon fatty acid which is implicated in modulation of gene expression and induction of apoptosis. Our results on *in vivo* effect of BuA indicates that it is not cytotoxic but it inhibits proliferation of Ehrlich Ascites Tumor (EAT) cells. The inhibition of proliferation was attributed to BuA-induced apoptosis of EAT cells, based on our results on Giemsa staining that exhibited apoptotic of EAT -cells in the sub-G1 phase of the cell cycle. Our results on the mechanism of BuA-induced apoptosis has revealed the specific induction of phosphoprotein phosphatase gene expression by BuA. Inhibition by sodium orthovanadate of the enzyme activity supports the view that a tyrosine phosphatase is induced by BuA. Inhibition of phosphatase activity also inhibited endonuclease activity suggesting that the endonuclease is regulated by dephosphorylation process. Currently BuA-induced death-signal transduction pathway is being elucidated.

118

USEFULNESS OF 'COMET ASSAY' IN PREDICTING REVERSIBILITY OF MONOCROTOPHOS INDUCED EFFECTS ON MICE BY VITAMIN E

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A sensitive and quick diagnosing single cell gel electrophoresis (comet assay) technique is used to visualize individual cells for their various levels of DNA damages caused by antibiotics, pesticides, apoptotic cells, nerotic states, cancer, aging, environmental pollutants etc. To test the reversibility of mutagenic effects of monocrotophos by Vitamin E, the adult albino mice of laca strain were administered vitamin E and monocrotophos by intragastric intubation at the concentration of 100mg/kg.b.wt. and 3.6mg/kg.b.wt. (i.e 1/5th of LD 50 dose) respectively for one month. The respective control groups were also maintained and treated the same way (only deionized water, only MCP or only vitamin E). To study the *in vivo* effects the multiple organs (kidney, spleen, liver and lung along with peripheral blood) were subjected to comet assay. The MCP treated animals showed largest comet tails in spleen and least in lungs. In the decreasing order the effect was observed in liver, kidney and peripheral blood. In MCP and vitamin E treated group , the tail lengths of the comet were reduced considerably there by showing that vitamin E acts as an antioxidant and protects tissue lipid from free radical attacks , repairs the damage caused by the metabolites of the pesticide, thereby decreasing the size of comets. It is suggested that the persons exposed to monocrotophos be given the dose of vitamin E in order to reverse the mutagenic effects of the pesticides.

✓ 119

STUDY ON SEXUAL SELECTION AMONG THREE CLOSELY RELATED MEMBERS OF SULFURIGASTER COMPLEX OF DROSOPHILA NASUTA SUBGROUP

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Mating perference experiments were conducted by providing both male and female choices among three closely related members of *sulfurigaster*

complex of *D. nasuta* subgroup namely *D.s. sulfurigaster* , *D.s. albostrigata* and *D.s. neonasuta*. Eight different crosses (employing unmated males and virgin females) were conducted in multiple replicates in similar conditions and total number of inseminations was recorded. Females were isolated and kept in fresh culture vials to allow egg laying. Glue protein samples from the third instar larval progeny of the inseminated females were prepared and analysed by way of SDS -PAGE to determine whether the mating is conspecific or heterospecific. Data obtained was pooled up and the percentages of conspecific or heterospecific. Data obtained was pooled up and the percentages of conspecific or heterospecific matings in each cross were calculated. Based on the results obtained in the present study, it could be proposed that *D.s sulfurigaster* is ancient among the members and *D.S. albostrigata*, derived. However, based on the isolation indices, it is concluded that the members under the study are still in the level of free inbreeding and are in the process of sexual divergence and hence, there is no sexual isolation.

120

FUNCTIONAL PROTEINS OF THE DEVELOPING BRAIN : NEUROTOXIC IMPACT OF THE INSECTICIDE METHY PARATHION AND PERMETHIN IN A DEVELOPING VERTEBRATE MODEL.

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Calcium binding regulatory protein calmoddulin and brain specific S-100 protein are known to have a strategic role in the efficient functioning of the nervous system. A comparative study of the alterations occurring in these two acidic proteins during pesticide toxicosis, revealed a general decrease in their levels. The synthetic pyrethroid, permethrin caused more decline in these two proteins compared to the effect of methyl parathion (organophospara), suggesting higher degree of toxic impact of pyrethroids.

Contrary to above observations, the total RNA , total protein content and the charged proteins exhibited a general stimulation on pesticide trament. However, phosphodiesterase activity showed a signigicant decrease. In view of these facts it can be presumed that pesticidal impact is causing disruptions in molecular mechanisms by affecting profoundly the functional proteins in a developing brain.

121

MORPHOGENETIC, BEHAVIOURAL AND BLOOD GROUP VARIATION AMONG FOUR ENDOGAMOUS GROUPS OF NORTH WEST INDIA

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The distribution of morphogenetic traits viz., ear lobe attachment and colour vision; behaviour traits viz., ABO and Rh (D) blood groups systems has been reported among four endogamous groups of north west India viz. Bawaria, Dakaut, Khatik and Meena. All the traits showed homogeneous distribution. The frequency of allele ranges from 0.122 to 0.270, that of B allele varies from 0.246 to 0.349 and O allele ranges from 0.400 to 0.571. The frequency of d allele varies from 0.200 to 0.282 and that of D allele ranged from 0.718 to 0.859. The present range of frequencies of traits falls well within the range for other populations of north west India.

122

POPULATION GENETICS OF HARYANA POPULATION

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In the present study, the distribution of morphogenetic traits viz., ear lobe attachment and colour vision; behavioural traits viz., hand clasping, arm folding, handedness and leg folding has been reported among five endogamous groups of Haryana state viz., Ramdasia, Jain (Banas), Bairagi, Chadha, (Panjabi Khatri) and Sansi. Among these traits, hand clasping, arm folding, handedness and leg folding showed significant differences ($.05 < P$). Ear-lobe attachment showed homogeneous distribution, while hand clasping, arm folding, handedness and leg folding showed heterogenous distribution. The frequency of these traits showed slightly higher range in the upper maxima as compared with the range for other populations of north west India.

MORPHOGENETIC AND BEHAVIOURAL VARIATIONS AMONG SIX ENDOGAMOUS GROUPS OF HARYANA

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As many as 82 communities, most of which are widely distributed, constitute the human populations of Haryana. The data are provided on the distribution of morphogenetic traits : ear-lobe attachment and colour vision, behavioural traits : hand -clasping, arm-folding and handedness and leg-folding among six endogamous groups of Haryana viz. Joginath, Panchal, Dakaut, Nai, Koli and Pal-Gadaria. Among these traits, ear-lobe attachment and handedness showed significant differences. Hand -clasping, Arm-folding and leg-folding showed homogeneous distribution while ear-lobe attachment and handedness showed heterogeneous distribution. No sampled individual among the caste groups investigated showed colour blindness. The frequency of traits studied presently falls well within the range of other caste groups of North -West India. The chi-square values for total group were found to be significant for ear-lobe attachment ($X^2 = 37.32$, $df = 5$, $0.01 < P$) and handedness ($X^2 = 33.74$, $df = 5$, $0.001 < P$) and non-significant for hand clasping ($X^2 = 2.87$, $df = 5$, $.95 < P < 50$), arm folding ($X^2 = 9.403$, $df = 5$, $.10 < P < .05$) and leg -folding ($X^2 = 1.46$, $df = 5$, $.95 < P < .50$)

CYTOGENETIC STUDIES IN PRIMARY AMENORRHOEA

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Primary amenorrhoea is a condition in which a female even at puberty fails to menstruate. Menstruation is directly linked with fertility of a woman, so in the absence of menstruation, the female shall be infertile. Primary amenorrhoea is a feature of Turner syndrome who are the females with abnormal sex-chromosome constitution (XO); however, primary amenorrhoea has also been reported in some females who are phenotypically normal.

In the present work, cytogenetic study has been carried out in fourteen females with primary amenorrhoea. Cytogenetic studies in these females showed chromosomal abnormalities like.

45, X.,
46.XX/45X;
46,XX/45,X/47, xxy;
46,XX/47, xxx ;
45,X/47,XX(trisomy 21,)

Sex chromosome mosaicism especially 46, XX/45, X has been found to be the commonest in majority of the cases.

125

CYTOGENETIC STUDY IN HUMAN CONGENITAL ANOMALIES

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The term congenital anomalies refer to the abnormalities existing from birth. They include variety of malformations, which are either due to :

a) Chromosomal changes

b) Environmental changes 'in utero' or otherwise of the two , the chromosomal changes are the most impotant cause of human congenital anomalies. These chromosomal changes may be numerical or structural or both , but in either case, these have adverse effects on the development of the foetus and latter has a variety of developmental abnormalities.

The study of the literature shows that the Down syndrome is the commoest human syndrome affecting 1/600 to 800 live births in general population all over the world, where in India it is estimated to be 1.09 in 1000 live births.

During present work, chromosome study has been carried out in 14 cases of children born with congenital anomalies. Through chromosome study , the incidence of trisomy-21 was found to be highest. Besides trisomy-21, other chromosomal abnormalities have also been recorded. In some cases, no chromosomal change could be seen and congenital anomalies in the child were attributed to some unknown environment al agent.

IN VITRO RADIATION PROTECTION OF HUMAN LYMPHOCYTE CHROMOSOMES AND FREE SCAVENGING BY ORIENTIN AND VICENIN

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Orientin (Ot) and vicienin (Vc) are two water soluble flavonoids isolated from the leaves of Indian holy basil *Ocimum sanctum*. These compounds increased the 30 days mouse survival after lethal whole body gamma irradiation (Uma Devi et al. 1999) and gave higher protection to mouse bone marrow chromosomes than WR-2721 and MPG in terms of toxicity and effective dose (Uma Devi et al. 1998). Therefore, the radioprotective effect of Ot and Vc against radiation induced chromosome damage in cultured human peripheral lymphocytes was studied. The possible antioxidant activity of these compounds was also tested *in vitro*. In order to select the most effective drug concentration, fresh whole blood was exposed to 4 Gy of cobalt-60 gamma radiation alone (RT) or with 6.25, 12.5, 15.0, 17.5, or 20.0 μ M of Ot/Vc for 30 min before RT and incubated at 37°C in RPMI. Cytochalasin B was added after 48h and cells were harvested after 72h of incubation. Cells were processed for micronuclei (MN) assay, fixed in methanol-acetic acid and stained with acridine orange. MN in cytokinesis-blocked lymphocytes were counted under fluorescence microscope. Pretreatment with either Ot or Vc at all concentrations significantly ($p < 0.05-0.001$) reduced the MN count. There was a concentration dependent increase in the effect, which was not significant above 17.5mM. Therefore, fresh blood samples were incubated with 17.5 mM Ot/Vc for 30 min and then exposed to 0.5-4Gy of gamma radiation. Another set of samples exposed only to 0.5-4 Gy of radiation served as control. Radiation increased the MN frequency linearly ($r^2=0.99$) with dose. Ot/Vc significantly ($P < 0.01-0.001$) reduced the MN counts to 51-67% of RT alone values. The reduction was proportional to the extent of damage observed at each radiation dose. At doses below 3 Gy, cells contained mainly one MN but cells with more than one MN increased with higher doses. Ot/Vc reduced the latter to about 50% of the RT alone values, suggesting that both compounds protected against multiple aberrations. Antioxidant activity of these compounds at concentrations of 0.25 -12.5mM was studied by measuring the inhibition of thiobarbituric acid reactive substance (TBARS) in Fenton reaction *in vitro* (Elizabeth and Rao 1990), with DMSO as the positive control. Both compounds produced

significant inhibition of TBARS which increased linearly with drug concentration. This activity was significantly higher than that of DMSO at equimolar concentrations. Thus, the results demonstrate that both the flavonoids possess significant protective activity against the clastogenic effect of radiation at low, nontoxic concentrations. The radioprotection seems to be associated with their antioxidant activity. The clinical potential of these protectors in cancer therapy needs to be investigated.

127

CYTOGENETIC ANALYSIS OF AMENORRHEA

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During the period of May 1999 to November 2000, sixty-one cases of amenorrhea have been referred to Division of Human Genetics, Department of Anatomy, St. John's Medical College, Bangalore for karyotyping and counseling. Among them 47 had normal karyotype (46,XX) and 14 had abnormal karyotype. Numerical abnormality was observed in 13: mosaicism - 10 (45, X/46, XX-4; 45,X/46,XY -3; 45,X46,XX/47, XXX - 3), 46, XY female -2 and 45, X -1; Structural abnormality was found in one (Iso X with increased heterochromatin material on 15 short arm). These patients and their family have been advised to have regular follow up.

128

RECIPROCAL TRANSLOCATION 46, XX, T (15; 22) ASSOCIATED WITH BOH

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A non-consanguineous couple aged 33/35 years was referred to the Division of Human Genetics, St. John's Medical College for karyotyping and counselling. The obstetric history showed 3 conceptions with blighted ovum and missed abortions. The husband's karyotype was 46, XY, while the wife's was 46, XX, t (15; 22) (q22;q13). Investigations done and the genetic counselling given are presented.

ANALYSIS OF SPUTUM CYTOLOGY AMONG STONE CRUSHER MILL WORKERS IN ORISSA

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Sputum samples from the occupationally exposed workers to dusts employed in stone crusher mills of Orissa were screened cytologically , since they are prone to many health hazards including lung cancer. In the present study, sputum samples from both non-exposed people (control) and stone crusher mill workes (experimental) were collected and fixed as per routine cytological procedure. The sputum samples were stained with Papanicoaou staining technique. No cytological abnormality was recorded in the sputum samples of control group while cytological screening of the sputum samples from 18 individuals out of 120 workers (includes both male and female belonging to age group between twelve to fitfty years and with exposure period of five to twenty years) of twelve different stone crusher mills exhibited cancerous conditions like keratinizing squamous cell carcinoma, keratinizing and non-cat cell carcinoma and adenocarcinoma. Preventive measures were suggested for the workers who are supposed to be with high risks of lung cancer.

A STUDY OF DIFFERENT FACTORS PROMOTING CARCINOMA ESOPHAGUS

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The incidence of Esophageal Carcinoma has increased substantilly in the last two decades. This increase may be largely attributed to the changing lifestyles of the people. Present study has been carried out with the aim to investigate the suspected factors which may be held responsible for causing carcinoma esophagus. Various factors considered for the present study are Age, Sex, Dietary habits and Socio-economic status and blood groups. Each one of these factors has been found to be influencing carcinoma esophagus directly or indirectly.

The results of the study will be discussed.

ANTIANGIOGENIC STRATEGIES TO INHIBIT TUMOR GROWTH AND ASCITES FORMATION IN EHRlich ASCITES TUMOR BEARING MICE: TARGETING VASCULAR ENDOTHELIAL GROWTH FACTOR BLOCKADE

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Malignant ascites is the accumulation of plasma -rich exudates due to tumor spread in the peritoneal cavity. Vascular endothelial growth factor (VEGF) or Vascular permeability factor (VPF) is a cytokine produced mainly by tumor cells and is responsible for leakage of the vasculature and proliferation of vascular endothelial cells and angiogenesis. The angiogenic actions of VEGF are mediated via two endothelium -specific receptor tyrosine kinases, Flt-1 and Flk -1/KDR. Targeting VEGF blockade is the main criteria of our work. Our results show that 0.5ng of VEGF/ microgram of protein is secreted into the ascites fluid of mouse bearing EAT-cells as measured by VEGF -sandwich ELISA. We have identified that sodium butyrate (a four carbon fatty acid) and curcumin (the active principal from turmeric) inhibited the expression of both VEGF mRNA and flt -1 m RNA by northern blot analysis , using labelled VEGF -cDNA as a probe. Using antiangiogenic compounds for therapy may be one of the strategies to inhibit tumor growth and ascites formation. However, we have also addressed the question whether blockade of angiogenic pathway by use of soluble receptors to trap VEGF and reduce the availability of VEGF to bind to its endogenous receptors will reduce tumor angiogenesis and ascites formation. The cDNA for the soluble receptors Flt-1 was subcloned into pCEP-4 vector. The EAT cells were stably transfected by standard calcium phosphate precipitation method. The clones were selected in hygromycin containing medium. The clones expressing maximum amount of the soluble receptor mRNA as measured by RT-PCR and soluble receptor protein, as measured by ELISA are chosen for further experiments. The selected clones are checked for difference in proliferation and growth in soft agar as compared to the wild type to make sure that *invitro* proliferation and the ability for anchorage independent growth are not compromised. The transfectants are currently being injected into Swiss nu/nu mice to verify if soluble Flt-1 gene therapy inhibits growth of EAT cells, ascites formation and peritoneal angiogenesis.

132

MOLECULAR MECHANISMS MEDIATING ANTIBIOTIC RESISTANCE -AN OVERVIEW

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Microbial resistance to antibiotic has emerged as a major hurdle in infection management. The rapid dissemination of drug resistance is principally mediated by a change in the bacterial DNA-occurring by either spontaneous mutations or transfer of resistance determinants between bacteria by DNA transfer. Gene transfer may occur by several mechanisms – extraction or lysis (transformation), through bacteriophage (transduction) or conjugation. The mobile genetic elements mediating drug resistance are principally plasmids (extra chromosomal , self replicating DNA elements) and transposons. The cellular resistance mechanisms involved include altered penicillin binding protein (PBP) , altered ribosomal proteins, altered acetyl transferases and others. Molecular research should facilitate early diagnosis and investigation of drug –resistant organisms in order to prevent drug resistance.

133

CYTOGENETIC EFFECTS OF OCCUPATIONAL EXPOSURE TO LOW-LEVEL IONIZING RADIATION IN RADIOGRAPHERS

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It is well known fact that radiation source is one of the most important diagnostic and therapeutic tools in the field of medicine and X-rays are the most effective and accepted means of diagnosis for several human ailments. Due to increasing use and no proper protective measures, the radiographers are occupationally exposed to low level ionizing radiations. Thus cytogenetic effects in 58 radiographers including 35 nonsmokers and 23 smokers working in four different hospitals in Hyderabad were evaluated by analysing chromosomal aberrations in the peripheral blood lymphocytes. For comparison, 82 control subjects consisting of 57 nonsmokers and 25 smokers, belonging to the same age group and socio-economic status but with no exposure to any physical or chemical agent at work place were also studied.

The lymphocyte cultures were carried out and slides were prepared using the standard method of Moorhead et al. Chromosomal aberrations like gaps, breaks, acentric fragments, exchanges, dicentrics, translocations and polyploids were observed in the exposed group. A significant increase in the frequencies of chromosomal aberrations was observed in nonsmokers (5.25) and smokers (8.14) of the exposed group when compared to the respective control groups (0.50, 3.12).

134

CYTOMORPHOLOGICAL STUDIES IN VICTORY 1 - AN IMPROVED VARIETY OF MULBERRY (MORUS L.)

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Recently evolved Mulberry (*Morus* L.) hybrid variety Victory 1 (V1) is being cultivated under varied agronomical conditions. In this variety, a few chimeric features such as disturbed phyllotaxy (opposite and whorl type of leaf arrangements), irregular leaf shape, size and internodal length, forked laminae and petioles, flattened shoots and mixed type of inflorescences were recorded in varied frequencies in 2-3 year old gardens.

Mitotic studies indicated that the variety is diploid with chromosome number $2n=28$. Meiosis was normal in male flowers produced by normal shoots. But meiotic irregularities such as 1-2 tetravalents, laggards, cytomixis and low pollen fertility were recorded in the male flowers produced by chimeric shoots. These cytomorphological variations are discussed in view of the type of chimerism existing in this variety.

135

GENETIC DIVERSITY AMONG THE ISOLATES OF MICROSPORIDIAN NOSEMA BOMBYCIS

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Microsporidia are obligate intracellular protozoan parasite which infect a wide range of invertebrates and vertebrates. The molecular karyotyping by

pulsed field gel electrophoresis, polymerase chain reaction, western blotting and bioassay of the *Nosema bombycis* isolates from infected silkworm *Bombyx mori* show the existence of avirulent strain and virulent strain. The dimorphism, the antigenic variation/processing and outbreak of pebrine disease caused by the *Nosema bombycis* once in every four years suggests the possibility of conversion of the avirulent stage to virulent stage during the life cycle of *Nosema bombycis*.

136

MEAN PERFORMANCE OF INTRA-RACIAL CROSSES OF PURE MYSORE INBRED LINES *BOMBYX MORI* L FOR SOME LARVAL TRAITS

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The pure Mysore inbred lines used in this study were collected from Bangalore (B), Bilidevalaya (BD), Magadi (M) and Mysore (My). The intra-racial crosses were made among the pure breeds and reared at Department of Sericulture, UAS, Bangalore. The highest hatching percentage (98.55%) was recorded by MyxB cross and least (93.86%) in MyxM cross. The reciprocal cross BDxMy and MyxM recorded significantly highest (93.14%) and lowest (90.13%) second instar larval progression, respectively. Whereas BDxB (93.48%) and MyxM (89.64%) reciprocal crosses recorded highest and lowest third instar larval progression, respectively. The reciprocal cross BDxMy (91.57,88.72%) and BxM (88.72,81.31%) recorded highest and lowest fourth and fifth instar larval progression. The direct cross MxB, MxMy and reciprocal cross BDxM exhibited lowest (266.66hr) and highest (276.00hr) fifth instar durations, respectively. The reciprocal cross BdxMy and direct cross MxB showed highest (760.33hr) and lowest (740.66hr) total larval duration, respectively. MyxM recorded least first (0.023g), second (0.131g) and third (1.087g) and highest fifth (20.57g) and mature larval weight (20.08g). BxBD and MxB exhibited highest (88.92%) and lowest (79.43%) ERR, respectively. The highest (1.007cg/day) and (1.066cg/day) productivity was obtained by BxBD and BdxMy, respectively.

PER CENT INCREASED/DECREASED VIGOUR OVER STANDARD CHECK VARIETY IN INTRA-RACIAL CROSSES OF PURE MYSORE SILKWORM FOR FEW GRAINAGE TRAITS

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The mean values of the 12 inter-regional crosses of Pure Mysore were compared individually with the standard check variety (Pure Mysore, CSR & TI) for the grainage traits and expressed in percentages. The results showed that there was no significant increase or decrease over standard check variety for moth emergence. Negatively and highly significant sex ratio of 95.18 per cent was recorded by My x BD and all the reciprocal crosses registered non-significant increase for sex ratio. The cross B x My (1.52%) B x M (1.62%) and BD x My (0.76%) showed non-significant increase and the remaining crosses showed highly significant increased vigour for fecundity. The cross B x My (27.90%) and My x M (23.25%), BD x M (18.60%) and My x B (30.02%) recorded significant increased vigour over standard check for egg diameter. There is no significant difference between crosses for weight of eggs. The direct cross M x B (-4.75%) M x My (-3.42%) and M x BD (-3.81%) recorded decreased egg weight. Whereas, My x B (2.94%) cross showed significant increased vigour over standard check for the number of eggs per ml ampule. The results revealed that the crosses with Magadi and Bangalore breeds performed better for the grainage traits.

APPLICATION OF COMBINING ABILITY AS A TOOL TO IDENTIFY THE BEST COMBINERS FOR COCOON AND SILK TECHNOLOGICAL TRAITS

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The study comprised of twenty crosses formed out of five lines viz., Pure Mysore (PM), MH1, Nistari (GY), BL-24 and SLKSPM and four testers viz., NB₄D₂, CSR-4, CSR-5 and NP₂ by crossing in line x tester system. The general combining ability and specific combining ability served as tool to identify the best combiners and best hybrids for the traits viz., cocoon yield

by number and weight /200 larvae, single cocoon weight, single shell weight, cocoon shell ratio percentage, single cocoon filament length, denier, reelability and raw silk percentage. Among lines MH1 was good general combined for single cocoon, shell weight, single cocoon filament length and reelability percentage followed by the BL-24 for cocoon yield by weight / 200 larvae, cocoon shell ratio percentage and raw silk percentage. Among testers CSR-5 was good general combiner for single shell weight, cocoon shell ratio percentage and reelability percentage followed by CSR-4 for single cocoon weight and denier. Among crosses, PM x NP₂ showed the highest specificity.

139

ESTIMATION OF EXTENT OF HETEROSIS FOR LARVAL AND GRAINAGE TRAITS IN NEW POLYVOLTINE X BIVOLTINE CROSSES OF SILKWORM *BOMBYX MORI* L.

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Five polyvoltine silkworm breeds viz., Pure Mysore (PM), MH₁, Nistari (GY), BL-24 and SLKSPM and four bivoltine breeds viz., NB₄D₂, CSR-4, CSR-5 and NP₂ were crossed in line x tester analysis system. Estimation of relative heterosis, heterobeltiosis and standard heterosis for single matured larval weight, total larval duration, effective rate of rearing, single pupal weight, rate of moth emergence, productivity and fecundity were computed. The hybrid BL-24 x NP₂ exhibited desirable negative relative heterosis, heterobeltiosis and standard heterosis for single matured larval weight, total larval duration and for single pupal weight, productivity and fecundity. The hybrid MH₁ x NB₄D₂ exhibited desirable relative heterosis, heterobeltiosis and standard heterosis for single mature larval weight, total larval duration, effective rate of rearing, productivity and fecundity. The hybrid MH1 x CSR-5 exhibited highest heterobeltiosis and positive standard heterosis for productivity.

STUDIES ON COMBINING ABILITY OF NEW SILKWORM BREEDS FOR LARVAL AND GRAINAGE TRAITS

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General combining ability and specific combining ability effects were studied for larval and grainage traits in five polyvoltine [Pure Mysore (PM), MH1, Nistari (GY), BL-24 and SLKSPM] and four testers (NB₄D₂, CSR-4, CSR-5 and NP₂) and 20 polyvoltine x bivoltine hybrids of silkworm *Bombyx mori* L. through line x tester system. Among lines MH1 was good general combiner for single matured larval weight, productivity, single pupal weight and rate of moth emergence percentage followed by PM for the fecundity and effective rate of rearing percentage. Among testers, NB₄D₂ showed highest *gca* effects for single matured larval weight and effective rate of rearing percentage followed by NP₂ for total larval duration. Among crosses, SLKSPM x CSR-4 recorded highest *sca* effects for single matured larval weight and rate of moth emergence percentage, MH1 x CSR-4 for fecundity, BL-24 x NB₄D₂ for total larval duration, MH₁ x NB₄D₂ for effective rate of rearing percentage, MH₁ x CSR-5 for productivity and PM x CSR-5 for single pupal weight.

HETEROTIC PERFORMANCE AMONG SOME MULTIVOLTINE X BIVOLTINE HYBRIDS OF SILKWORM BOMBYX MORI L FOR GRAINAGE TRAITS

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Search was made for elite genotypes of silkworm *Bombyx mori* L. for seed technological traits based on heterosis among 28 hybrids synthesised from seven multivoltines viz., Pure Mysore (PM), Thai, P₂D₁, Hosa Mysore (HM), Nistari, Kolar Gold (KG) and Kollegal Jawan (KJ) and four bivoltine

breeds viz., NB_4D_2 , NB_{18} , KA and NP_2 in line x tester crossing system. The cross $P_2D_1 \times NB_{18}$ in general manifested higher significant positive better parental heterosis for grainage traits i.e., pupal weight, rate of pupation and moth emergence. The crosses KJ x NP_2 and KG x KA registered higher positive significant heterosis over better parents and standard check for fecundity.

142

APPROPRIATE SELECTION OF HYBRIDS OF SILKWORM (BOMBYX MORI L.) THROUGH HETEROSIS BREEDING FOR REARING TRAITS

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Search for suitable hybrid combinations of silkworm (*Bombyx mori* L.) for rearing traits was made among 28 F_1 hybrids synthesised from seven multivoltine and four bivoltine silkworm breeds in line x tester fashion through heterosis breeding. The cross HM x NB_{18} ranked top for extent of progression of fourth instar and effective rate of rearing by yielding significantly positive heterobeltiosis and standard heterosis for full grown larval weight. The hybrid $P_2D_1 \times NB_{18}$ recorded highest negative standard heterosis for fifth instar and total larval duration. The rearing traits viz., extent of progression to fourth instar, larval duration upto fourth instar, fifth instar duration, total larval duration, full grown larval weight and effective rate of rearing revealed that the hybrids, $P_2D_1 \times NB_{18}$ and KJ x KA manifested significantly higher standard heterosis in desirable direction. It is very interesting to note that the crosses with P_2D_1 and NB_{18} as lines and testers, respectively produced highest standard heterosis for rearing traits in general.

143

CHANGES IN REDUCING SUGAR CONTENT IN THE EXCRETA DURING LARVAL DEVELOPMENT OF THE SILKWORM BOMBYX MORI L

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The level of reducing sugar in the excreta during larval development of bivoltine race and cross breed of *B. mori* was studied. Both the varieties of silkworm studied, showed almost the same trend in the level of reducing sugar in the excreta during the complete larval life. The level of reducing sugar increased on first and second day during I instar, from first day to third day during II instar and first day to fourth day during III instar and decreased thereafter till the end of the instar. During IV instar, the level of reducing sugar increased upto third day, decreased on the fourth day and again increased slightly on fifth day. During V instar, it increased upto third day, decreased upto sixth day and followed by an increase till the end of V instar. The results are discussed in relation to the changes in the absorption of carbohydrates and the physiological activities in the body of the silkworm larva.

144

CYTOTAXONOMIC INVESTIGATIONS IN SOME MULBERRY CULTIVARS

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Mulberry, the sole food plant of silkworm *Bombyx mori* L. is of great economic importance to the sericulture industry. The major problem hindering the progress in improvement of mulberry is lack of information on cytogenetic aspects. Nevertheless, not much is known about the genetic built of the genotypes, being handled by the breeder. Inheritance pattern is not known for many agronomic traits, which is rather basis for conventional methods of plant improvement. In addition, the information on some basic aspects like-systematics, cytogenetics, heterosis, etc., are scanty. Mulberry being highly cross pollinated offers ample scope for studying genetic diversity. Keeping all these in view, an attempt has been made to examine four mulberry cultivars viz., S₄₁, Berhampore local, Kosen and Kajali from the morphological and cytological point of view. In the present investigation, the taxa studied resemble in their gross morphological characteristic features like habit, branching pattern, alternate phyllotaxy, catkin inflorescence, multicostate-reticulate leaf, yet they differed significantly in several micromorphological features. The somatic chromosome number of Kosen, Berhampore local and Kajali was found to be 2n=28. The haploid chromosomes number of n=23 was observed in S₄₁ variety.

EVALUATION OF SELECTED MULBERRY GERMPLASM RESOURCES TO DROUGHT TOLERANCE IN KOLAR DISTRICT OF KARNATAKA STATE-ROOT PROLIFERATION STUDIES

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Based on the morpho-anatomical parameters , six mulberry germplasm accessions, presumed to be stress tolerance to drought is selected from among the 328 mulberry germplasm resources collected from all over the country. Field testing of these six mulberry accessions in the drought prone/stress tolerance area of Kolar District during 1999-2000, showed the root proliferation in these varieties to be highly significant over the ruling K-2 variety, 14.21 ml/plant over check variety Kanva-2 for (or K-2) with 4.17 ml/plant. However, the root length varied among the test varieties, longest root length was recorded in MI - 0078 with 25.99 cm followed by MI - 0195 (23.57cm) , MI 0004 (22.00 cm) and check variety MI-0014 with 16.06 cm. Present study also showed that the morpho-anatomical parameters based selection of mulberry varieties for stress tolerant and drought prone areas is a more reliable method.

STUDIES ON MINERAL CONTENTS IN DIFFERENT SPECIES OF TERMINALIA

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In the present investigation , six species of *Terminalia* Viz ., *Terminalia tamentosa* W & A., *Terminalia arjuna* W&A., *Terminalia chebula* Retz., *Terminalia bellerica* Roxb., *Terminalia paniculata* Roth., and *Terminalia catappa* Linn., the food plants of tropical tasar silkworm *Antheraea mylitta* D were analysed for different inorganic mineral contents viz., Nitrogen, Phosphorus, Potassium, Calcium, Magnesium, Sulphur, Zinc, Copper, Iron and Managanese. The taxa studied exhibited notable variations in these constituents quantitatively. Further, these plant species also showed variations in distribution pattern and exomorphic features.

CHARACTERIZATION OF HEAT SHOCK PROTEINS IN SILK-WORM, *BOMBYX MORI* L

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Insects respond to sudden increase in temperature (Heat Shock response) by synthesizing a small set of proteins called heat shock proteins (hsps). This heat shock response has been highly conserved throughout the evolution, not only as a physiological phenomenon, but also at the level of individual proteins. Heat shock proteins comprise some of the most highly conserved protein families known. A study was initiated to study the genetic basis of heat shock response in different varieties of silkworm such as diapausing and non-diapausing. Silkworm larvae (Fifth instar) were subjected to different temperatures ranging from 28°C to 41°C. After heat shock treatment, five novel proteins of molecular weight hsp 100, hsp 90, hsp 69, hsp 60 and hsp 29 Kda were synthesised and the protein hsp 69 Kda was found to be predominant in the silkworms studied. The preliminary results suggests the differential expression of hsps in diapausing and non-diapausing silkworm varieties, which shall be discussed.

IRRIGATION OF MULBERRY WITH SEWAGE WATER AND ITS IMPACT ON SILKWORM (*BOMBYX MORI*) REARING

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The major factors which determine the productivity inturn profitability in sericulture are the yield and quality of mulberry leaves which have a predominating influence on silkworm and cocoon crop. The chemical composition of mulberry leaves depends on various factors like soil, fertilizer, irrigation, pruning season, maturity etc. Among these, irrigation plays a pivotal role not only in the higher yield of mulberry leaves but also on the cocoon crop. A study was carried out to assess the nutritional status of mulberry leaves from the gardens irrigated with vrishibhavathi river water (In 5 different points) polluted by domestic and industrial effluents vis-a - vis analysis of heavy metals in water and nulberry leaves. The garden

irrigated with bore-well water is considered as control. The sewage water and mulberry leaves (Irrigated with sewage water) analysis showed the possession of higher percentage of heavy metals which feasibility of utilisation of sewage water and its impact on silkworm rearing will be discussed.

149

EVALUATION OF SOME EXOTIC MULBERRY GENOTYPES FOR GROWTH AND LEAF YIELD

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Six exotic mulberry genotypes viz., Papua New Guinea, Okinawa-2, Philippines, Goshierami, Tai song-3 and Thailand maintained in the germplasm bank at Bangalore university, Bangalore were utilized for the study. These genotypes were planted at a spacing of 90x90 cm under irrigated system. After the initial establishment for 3 years, the genotypes were evaluated for growth and leaf yield parameters for one year and compared with Kanva-2 grown under similar conditions. Pooled data of four crops showed significant differences in yield and yield attributing characters among the genotype. Leaf yield was maximum during Jun-Aug and Sep-Nov crops. Papua New Guinea was found superior to other genotypes in most of the yield attributing parameters over four leaf harvests. Papua New Guinea recorded leaf yield of 4294.3g/plant/ crop as compared to only 2434.2g/plant/crop in case of Kanva-2, while Tai song-3 recorded a leaf yield of 2247.04g/plant/crop. Based on the performance with respect to growth and leaf yield, Papua New Guinea can be considered as potential genotypes for cultivation under irrigated conditions.

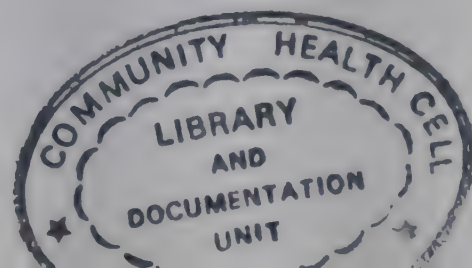
150

IMPROVEMENT OF SILKWORM BREEDS BY ISOZYME MARKER ASSISTED SELECTION

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In recent years, molecular markers are being widely explored for the improvement of desirable traits during the breeding of crop plants and live stock. In pursuit of suitable biochemical markers to be used in the silkworm breeding programmes, work carried out earlier has indicated the prospects



of using digestive amylase enzyme as a useful marker in silkworm breeding in view of its role in better digestibility, close association with survival and distinct isozyme polymorphism. As a follow up of this finding, a backcross breeding scheme was designed. Productive bivoltine breeds, viz, CSR2 and CSR5 were used as recurrent parents (RPs) and Near isogenic lines (NILs) were evolved by introgressing '4 band' and '5 band' amylase isozymes from indigenous polyvoltine breeds, namely, Pure Mysore and Nistari , respectively. The evolved NILs have shown significant improvement in survival over their respective RPs without any deterioration in yield traits. For identification of promising hybrid combinations for field testing, seven hybrid combinations of the evolved NILs were evaluated under six crops during 1998-99. Based on the evaluation index (EI) values, three promising hybrids were short-listed and tested under three trials during 1999-2000 at regional stations. The trials have indicated the superiority of the hybrid Gen 3xGen 2, in terms of higher EI values for survival and ten yield traits when compared to those of the control. The results have shown the prospects of employing isozyme marker assisted selection in silkworm breeding for improvement of target traits.

151

AN EASY AND SIMPLE METHOD OF EXTRACTION AND PURIFICATION OF GENOMIC DNA IN MULBERRY

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Mulberry genomic DNA has been extracted and purified from young leaves of 14 mulberry genotypes with three different extraction methods. Among the three methods tried, modified Dellaporta method (method 1) was found to be suitable for PCR amplification with high purity (A_{260} , A_{280} ratio varies from 1.936 to 1.829) and yield (396 ug/g to 321mg/g tissue) of genomic DNA. PCR amplification of genomic DNA extracted through the method 1 further confirms its purity.

RAPD MOLECULAR MARKER FOR GENETIC ANALYSIS OF MULBERRY ACCESSIONS

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The mulberry plants are dioecious and cross pollinated with each other to produce fertile hybrid indicating a closer genetic relationship, and is not identified at species level. The common methods using morphological traits are not very useful in establishing the relationship and diversity among different mulberry accessions. Because of the environmental influence, PCR method of molecular marker, RAPD was adopted to study the genetic diversity and interrelationship of 14 mulberry accessions/varieties (*M. australis*, Okinowa, Moulai, English black, China peaking, Shrim 2, *M. nigra*, PKS1 -4, Japan -11, Philippines, PKSI -11, Paraguay, PKSI-9 and Kamiso - 402) on an average, random amplified polymorphic DNA (RAPD) analysis generated 5 discrete DNA bands/accessions with five oligonucleotide primers. The size of the amplified products ranged from 300-5000 gp with an average of 2-6 bands for each primer. Majority of them is polymorphic (96%). RAPD analysis of identification and amplification products is useful in mulberry germplasm classification and introgression studies. Further, the results indicated that RAPD analysis of identification and amplification products is useful in mulberry germplasm classification and introgression studies. Further, the results indicated that RAPD molecular marker are useful in mulberry breeding and genetic level of characterization at species/accessions/varieties

RAPD ANALYSIS OF GENETIC VARIABILITY IN MULBERRY GERMPLASM (GENOTYPES)

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Seven mulberry varieties from mulberry germplasm were selected to find out the morphological and genetic variations. Phenotypic and genotypic variations in mulberry varieties viz., Farmer's house, Thysong, Philippines, Multicaulies, Kosen, M5 and Kajali. Apart from morphological traits and

root traits, genetic variation using RAPD markers Random amplified polymorphic DNA were carried out. The DNA of these varieties was extracted using the standard method of plant DNA extraction (modified potassium acetate method). The PCR amplification of DNA was carried out using standard PCR protocols. The study indicated that there was wide range of variation in both the morphological traits and at genetic levels using markers. Some of the DNA bands generated by RAPD markers technique had unique pattern specific to each variety, which could be obvious from the study of the RAPD markers used for identifying individual varieties. The DNA finger printing in mulberry is useful as compared with other crops to locate the right clones and also useful in avoiding duplication in germplasm and maintain purity and to study the evaluation of different ploidy species of mulberry in germplasm bank. The RAPD analysis offered a rapid and reliable method for the estimation of variability between different varieties which could be useful for breeders for further improvement in mulberry varieties.

154

ECONOMIC TRAITS OF NB₄D₂ AS INFLUENCED BY PROTEIN ENRICHED MULBERRY LEAVES

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Silk cocoon yield is controlled polygenically by quantitative characters which is the sum total effect of several component factors, the influence of which can be ascertained through correlation studies. Leaf enrichment with protein supplements contributes to added values of economic traits in silkworm. Correlation analysis was made for qualitative and quantitative traits of NB₄D₂ silkworm were reared on eight different proteins supplemented mulberry leaves.

The data on larval weight was correlated with the traits like ; larval volume, silkgland volume/weight/ratio, duration to ripen and effective rate of rearing (ERR). Cocoon weight was correlated with dry cocoon, pupal and shell weights, shell percentage, silk filament length , denier, fibroin and sericin percentage of the silk filament. Highly significant and positive correlation of mature larval weight with larval volume ($r=0.9381^{**}$) silkgland volume ($r=0.9258^{**}$), silkgland weight ($r=0.8986^{**}$) silkgland ratio($r=0.9021$)

and ERR ($r=0.8861^{**}$) with observed. Duration to ripen exhibited significant negative correlation ($r=0.9459^{**}$) with other qualitative traits. Highly significant and positive correlation of cocoon weight with dry cocoon weight ($r=0.9544^{**}$), pupal weight ($r=0.9966^{**}$), shell percentage ($r=0.9860^{**}$), filament length ($r=0.9905$) and sericin percentage ($r=0.9209^{**}$) were also observed. Denier ($r=0.9867^{**}$) and fibroin percentage ($r=0.9208^{**}$) exhibited significant negative correlation with other quantitative traits.

Enrichment of mulberry leaves with protein supplements strongly favoured the larval growth, development and cocoon productivity in NB₄ D₂ breed.

155

IDENTIFICATION OF COMPONENT TRAITS IN PURE MYSORE BREED FOR BREEDING PROGRAMME THROUGH PATH CO-EFFICIENT ANALYSIS

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Data generated in respect of economic traits of Pure Mysore (PM) silkworm breed reared on eight different protein supplements was subjected to Path Co-efficient Analysis (PCA). The PCA is useful in identifying the component characters of a genotype for breeding purpose. The PCA for qualitative characters of PM breed indicates that silkgland volume (0.5515), silkgland ratio (0.0400) and effective rate of rearing (ERR) exhibited positive direct effect on mature larval weight whereas, larval volume (-0.1054), silkgland weight (-1.5907) and duration to ripen (-1.2362) showed negative indirect effects. Among the quantitative traits, dry cocoon weight (0.0551), pupal weight (1.2776), shell weight (1.1880) and denier (0.5248) exhibited positive direct effect on fresh cocoon weight. However, shell percentage (-1.8704), filament length (-0.7122), fibroin content (-0.7450) and sericin content (-1.1913) showed negative direct effect. It is evident from the present finding that ERR, silkgland volume, silkgland ratio, pupal and shell weights and filament length were the most important component traits in PM breed and these traits need to be given emphasis while conducting breeding programme for higher cocoon weight.

156

EFFECT OF SUBLETHAL CONCENTRATION OF AN ORGANO-PHOSPHATE INSECTICIDE METHYL PATATHION ON BRAIN ACETYLCHOLINESTERASE ACTIVITY OF DEVELOPING BOMBYX MORIL

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The effect of sublethal concentration of methy parathion on the brain acetylcholinesterase (AchE.E.C. 3.1.1.7) activity of the fifth instar larvae of *Bombyx mori* L was studied. The effect of sublethal concentration of methyl parathion exposure (2.5 µg/2µl of acetone /larva) was determined in the soluble and membrane bound fraction of the brain and the kinetic characters like Km and V max were computed. The soluble and membrane fractions were susceptible to the toxic impact of methyl parathion and exhibited a differential response to methyl parathion exposure.

157

CYTOLOGICAL CHARACTERISATION OF MITOTIC AND MEIOTIC CHROMOSOMES OF SAMIA CYNTHIA RICINI

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The present investigation deals with the cytological characterisation of *Samia cynthia ricini* (Saturniidae : Lepidoptera), the domesticated eri silk worm. Mitotic (larval neuroblast cells) and meiotic (testes and ovary) chromosomes were prepared following the conventional air drying techniques (Chowdaiah and Venkatachalaiah 1987, Imai 1972) and the same were stained with Giemsa solution. The diploid chromosome number was found to be 28. Mitotic and meiotic kayotypes of both the sexes were prepared. Differential banding techniques such as C-and Ag-staining have been employed for the detailed characterisation of meiotic chromosomes of both sexes, in order to highlight the mode of pairing and the occurrence of heteropycnosis of the sex bivalent in the complement.

EVALUATION OF 12 MULBERRY GENOTYPES (*MORUS* SPP.) FOR HIGHER PRODUCTIVITY UNDER RAINFED CONDITIONS OF SOUTHERN INDIA

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To assess the yield potential, field trial of 12 mulberry genotypes (with S13 genotypes as check), under RBD, 4 replicates/genotype and 90 x 90 cm plant spacing, was carried out at the main campus of the KSSRDI, Bangalore, with a total of 18 harvests (1994-95 to 1996-97). The genotypes showed significant differences for all the four parameters studied and also with reaction to seasons. The fresh weight of 100 leaves ranged from 82.46 (Mysore Local) to 247.89g (Vishala). Genotypes Viswa (190.23g), RFS 135 (201.14 g), RRS 175 (195.27g), Sujanpur (166.25g) and MR 2 (163.98g) had highly significant values of fresh weight of 100 leaves when compared with S13 genotype (130.41g). The leaf water content (LWC) ranged from 69.17 (Mysore Local) to 73.60% (Viswa). Genotypes Viswa and Vishala (73.57%) had highly significant values of LWC compared with S13 genotype (72.54%). The leaf water retention (LWR) ranged from 79.57 (Mysore Local) to 86.55% (Vishala). Genotypes MR2 (86.10%) and Vishala had highly significant values of LWR , when compared with S13 genotype (84.34%) . The leaf yield /replicate /year ranged from 4.68 (Kadaganchi) to 11.13kg (Vishala). Genotype Vishala had highly signifincat leaf yield when compared with S13 genotype (8.91kg). The total nitrogen content also varied among the genotypes, ranging from 3.07 (Vishala) to 3. 68%(Kadaganchi).

The performance of genotypes decreased from rainy to summer through winter season to different extents and the differents were highly significant. When the performance of 12 genotypes was considered only for summer season, genotype Vishala tops the list, followed by Vishala genotype was best among the 12 genotypes , followed by Viswa genotype, under rainfed conditions.

THE CHIMERAL NATURE OF THE ENTIRE LEAF VARIANT IN THE MULBERRY GENOTYPE - MYSORE 5 (*MORUS INDICA* L.)

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A spontaneous chimeric mutant of the popular Mysore -5 genotype (M5 or K2 or Kanva -2 , cultivated extensively in South India, to conduct silkworm rearings) was collected from mulberry garden of a farmer, at Kadaganchi village, Gulbarga District, Karnataka. The genotype is a diploid ($2n = 28$) , mericlinal chimera, characterized by leathery dark - green, unlobed, leaves, with bullate texture and sharp-crenate margin. Based on the comparative study of this chimera, with normal M5 genotype , it has been observed that the chimera has higher plant height and longer internode length, less number of branches/plant , fresh weight of 100 leaves and rooting, when compared with M5 genotype. Also , in leaf anatomical parameters like leaf thickness, thickness of upper and lower epidermis, thickness of upper and lower cuticle, thickness of palisade and spongy parenchyma, stomatal frequency and stomatal length and width, the values were highly significant with respect to thickness of upper epidermis [(16.03 (M5) and 13.79 μm (chimera)] and stomatal frequency [537.21 (M5) and 742.87/ mm^2 (chimera)] and significant in thickness of lower epidermis [11.45 (M5) and 10.48 μm (chimera)] and palisade parenchyma [38.56 (M5) and 41.32 μm (chimera)]. The mutant can be referred as plastid gene-chimera and has no economic potential from the point of sericulture.

ON THE PRESENCE OF CALMODULIN IN THE BRAIN OF CONTROL AND METHYL PARATHION EXPOSED DEVELOPING SILKWORM *BOMBYX MORI* L

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Presence of calmodulin (CaM) in considerable amount in the V instar developing larvae of *Bombyx mori* L (PM x NB₄D₂) was found. CaM content exhibited a gradual increase from 1st day to 7th day of development in the V instar larvae. The CaM content in the brain of methyl parathion exposed

animals showed remarkable decline during development in the V instar. Involvement of the calcium binding regulatory protein calmodulin in cellular regulatory mechanisms during development is discussed.

161

EVALUATION AND SELECTION OF POTENTIAL BREEDS FOR HYBRIDIZATION STUDY

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In order to identify potential breeds to derive different combinations for hybrid testing, 12 multivoltine and 47 bivoltine breeds were evaluated under "multiple trait evaluation index". The mean data for ten metric traits such as fecundity, hatching, larval duration, cocoon yield by number, cocoon yield by weight, cocoon weight, cocoon shell weight, cocoon shell ratio, filament length and reelability were recorded, pooled for different seasons and analysed statistically to select potential breeds. On the basis of indices obtained for ten characters, 7 multivoltine breeds were selected as potential breeds and are placed in the order of merit viz., MG520, MG508, MU11, MU303, MY1 and PM. Among 47 bivoltine breeds, eight were selected as potential breeds and are placed in the order of merit viz., MU927, MG580, MU723, CC1, MU807, MG511, NB₄ D₂ and KA.

162

RACIAL VARIATION IN DIAPAUSE INDUCTION AMONG MULTIVOLTINE BREEDS OF INDIA

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Silkworm are classified as univoltines, bivoltines and multivoltines depending on the number of generations they undergo in a year under natural conditions. In general, uni and bivoltine are diapausing and multivoltine are non-diapausing in nature. However, diapause nature is also reported in certain multivoltine breeds during certain seasons.

In light of the above, the present investigation was carried out to study the response of different races to diapause induction using six multivoltine breeds. Treatments set up for diapause induction involved (1) Exposure of

silkworm larvae to 20°C from fifth instar to pupation and (2) Exposure of silkworm larvae to 20°C from spinning to pupation. Layings in which eggs developed pigmentation were scored as diapause layings.

Results of the study revealed that there was significant effect with regard to diapause induction between treatments and also breeds. Between treatments, the diapause laying % was higher (36-26%) when larvae were exposed to 20°C from fifth age to pupation (36-26%) when compared to exposure from spinning to pupation (19-35%) , while among breeds, BL23 recorded maximum diapause induction (64.97%) followed by PM (61.22%) whereas both the treatments could not induce diapause in layings of Nistari and Chalsa Nistari breeds.

It could therefore be inferred from the study that there is differential behaviour among multivoltine races to diapause induction.

163

GENOTYPE -ENVIRONMENT INTERACTION FOR SILK YIELD CONTRIBUTING CHARACTERS IN MULBERRY SILKWORM, *BOMBYX MORI*.

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42 strains of silkworm (*Bombyx mori*) of different geographical origin were evaluated for stability performance. Data of three seasons (autumn, spring and summer) during 1991-92 were analysed statistically for silk yield contributing characters viz., pupation rate, cocoon weight, shell weight, shell ratio and filament length by using regression method. The results indicated the significance of genotypes/ strains, environment and genotype x environmental interactions for their influence on all the five characters. Environmental index revealed that autumn (September -October) is the most favourable season for exploiting all the five characters. Considering the stability parameters, the most stable strains for different characters are as follows : strain NJ1 (cocoon weight , shell weight , shell ratio and filament length) : strains CB3P and SSOP (pupation rate shell ratio and filament length) strains Dong -306, NBI and SPCI (pupation rate filament length) ; strains 247 and JIM (pupation rate and shell ratio). The strains selected will be used in improving old strains and in developing new breeds and lines .

164

USE OF BUD POLLINATION AND MENTOR POLLEN TECHNIQUE TO OVERCOME PRE-FERTILIZATION BARRIERS IN INTERSPECIFIC CROSSES OF SESAME

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Interspecific crosses were made between *Sesame indicum* and its wild relatives viz., *S. occidentale*, *S. radiatum* and *S. mulalayanum*. Based on field pollination and *in vivo* pollen germination studies, the barriers to hybridization were identified and classified as pre-fertilization in the crosses involving *S. occidentale* and *S. radiatum* as male parents. However, in the crosses with *S. mulayanum*, viable F_1 s were obtained indicating absence of hybridization barriers. Different techniques like bud pollination and use of mentor pollen were attempted in the crosses showing pre fertilization barriers. In addition, an attempt was made to know the role of enzymes such as esterase and peroxidases and various macromolecules such as starch, polysaccharides, proteins and RNA/DNA in cross- (in) compatibility.

165

GENETIC AND POLLEN STUDIES IN GLADIOLUS SPP

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Variability studies among 35 *Gladiolus* genotypes [11 Indian and 24 exotic] for 30 characters conducted at the Indian Institute of Horticultural Research, Hessaraghatta, Bangalore during 1998-99 revealed that, all the genotypes exhibited wide range of variation for days for spike emergence, floret size, number of florets open at one time, number of florets per spike, spike length, rachis length and number of cormels per corm. For all the 30 characters studied, the differences between phenotypic and genotypic co-efficients of variation were narrow indicating less environmental influence on their expression. High phenotypic and genotypic co-efficients of variations, heritability and genetic advance recorded for number of shoots per plant, number of spikes per corm, number of daughter corm, number of cormels per corm and 25 cormel weight suggests selection of genotypes based on these traits for further improvement through effective breeding programmes.

Pollen from five *Gladiolus grandiflorus* varieties viz. Darshan, Dhiraj, Sagar, Sapna and Shobha developed at I.I.H.R. and *G. calliantus* a wild fragrant species were stored at - 65°C for three days and nine months and -196°C (in liquid nitrogen) for three days. The findings revealed negligible loss in the viability of pollen measured in terms of germination % *in vitro*, vigour (tube length) and fertility assessed through the number of seeds set per capsule upon pollination compared to fresh pollen. Since the above results also indicate no species/varietal/duration specific pollen storage temperature, establishment of 'Pollen Banks' would assist gladiolus breeders to overcome the problem of asynchronous flowering among the genotypes and would also aid exchange of germplasm.

A preliminary attempt was made to screen resistant (Dhiraj and Psittasinus hybrid) and susceptible (Friendship and Pricilla) genotypes for their resistance/susceptibility against *Fusarium* with through *in vitro* pollen studies. The result of the study are discussed in this paper.

166

NUCLEAR DNA CONTENT IN SOME *DENDROBIUMS*

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Dendrobium is the largest orchid genus comprising approximately 1000 identified species (Dressler 1993). The genus has a wide geographical distribution and has a high horticultural potential because of its diversity in form. Despite the large size and horticultural importance, it has received very little attention with regard to nuclear DNA content, referred to as C-value. Understanding the evolutionary significance of C-value is one of the major focus in contemporary plant molecular biology. This paper discusses the C-values in *Dendrobium* species and hybrids in an evolutionary perspective.

167

CYTOGENETIC DAMAGE IN INDIVIDUALS EXPOSED TO VEHICULAR POLLUTION

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Cytogenetic investigations on peripheral blood lymphocytes of 50 individuals exposed to different air pollutants on the road sides was made. This was compared to an equal number of exposed and matched controls w.r.t. age, sex, smoking and drinking habits and social status. The mitotic index (MI), chromosomal aberrations (CA), sister chromatid exchanges (SCE) and satellite associations (SA) were analysed. All the parameters showed a significant increase ($P < 0.01$) in the exposed sample compared with the controls, viz. MI, 3.75-6.80; CA 0.96-2.98; SCE 3.92-8.18 and SA 6.18-14.50. The occurrence of DG type of satellite association was highest and that of 3D type lowest. The frequencies of all the parameters also showed elevation with duration of exposure. MI, however, showed decrease after continuous increase upto 15 years of exposure. The vehicular fumes were thus found to be genotoxic.

168

STRUCTURAL CHROMOSOMAL ABNORMALITIES IN HUMAN CARCINOMA OESOPHAGUS

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Carcinoma oesophagus is a major health problem in J&K State and common malignancy found both in men and women in their sixth and seventh decades of their life. Its incidence is found to be higher (87%) in males as compared to that of females (33%). Chromosome study conducted in some of the histopathologically confirmed cases of Ca oeso showed complex patterns of chromosomal changes like deletion, breaks, endoreduplication etc.

169

A REPEATABLE PROTOCOL FOR THE PRODUCTION OF GYNOGENIC HAPLOID PLANTS IN MULBERRY

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Haploid plants have been obtained from unpollinated Gynoecium of Mulberry variety-S54 cultured *in vitro* as here reported for the first time. The shoot primordia and multiple shoots were produced after 4 and 8 week of explant culture respectively on LS+BAP (2mg/l) +Kn (1mg/l). Callus was not formed at any step of the process. The well developed gynogenic multiple shoots were transferred to rooting medium LS + BAP (2mg/l) +NAA (1mg/l). The gynogenic plants have been established in soil. The gynogenic plants were screened cy-

tologically and they showed the haploid number of chromosomes $n = 14$ in their root tips.

170

ISOLATION OF SOMACLONES IN ZINGIBER OFFICINALE ROSC

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Ginger is the underground rhizome of *Zingiber officinale* Rosc., belonging to the family Zingiberaceae and sub-family Zingiberoideae. Ginger has been prized since ancient times for its flavor and medicinal properties. Ginger is affected by various diseases of fungal, bacterial, viral and mycoplasmal origin. Of these, rhizome rot or root rot disease caused by *Pythium aphanidermatum* results in considerable crop loss. Somaclones have been isolated through direct and indirect regeneration using different explants on LS and MS media supplemented with different concentrations of Auxins and Cytokinins for callus induction. The callus was transferred to LS medium supplemented with 4 mg/l BAP for shoot multiplication. Further, somaclones were also isolated by treating the vegetative buds with chemical mutagens (Ethyl Methane Sulphonate and Sodium Azide) at different concentrations and at different time intervals on LS medium supplemented with 4mg/l BAP. The isolated somaclones were compared with control for different morphological parameters (leaf length, breadth, plant height and number of roots per plant). These somaclones were screened for disease resistance (root rot) by the direct application of the toxin (*Pythium aphanidermatum*) results in considerable crop loss. Somaclones have been isolated through direct and indirect regeneration using different explants on LS and MS media supplemented with different concentrations of Auxins and Cytokinins for callus induction. The callus was transferred to LS medium supplemented with 4 mg/l BAP for shoot multiplication. Further, somaclones were also isolated by treating the vegetative buds with chemical mutagens (Ethyl Methane Sulphoneate and Sodium Azide) at different concentrations and at different time intervals on LS medium supplemented with 4mg/l BAP. The isolated somaclones were compared with control for different morphological parameters (leaf length, leaf breadth, plant height and number of roots per plant). These somaclones were screened for disease resistance (root rot) by the direct application of the toxin (*Pythium aphanidermataum*) to *in vitro* plants.

171

QUALITATIVE AND QUANTITATIVE ANALYSIS OF MALE ACCESSORY GLAND SECRETORY PROTEINS IN A FEW MEMBERS OF NASUTA SUBGROUP OF DROSOPHILA

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In *Drosophila*, accessory gland secretory proteins are stage specific, tissue specific and sex specific. These proteins are transferred to the female during mating and are responsible for mating mediated changes in the female. By employing the laboratory stocks of *D.n. nasuta*, *D.n. albomicans*, *D. kohkoa*, *D.s. sulfurigaster*, *D.s. albostrigata* and *D. s. neonasuta* present investigations were carried out to analyze these secretory proteins qualitatively by way of SDS-PAGE and quantitatively by micromethod. Qualitative analysis revealed pattern variation with reference to low molecular weight protein fractions. Taking the advantage of cross fertility and differential patterns, the mode of inheritance of specific secretory protein fractions was studied. Analysis of profiles specific fractions in the interspecific F_1 males using volume analysis mode of molecular analyst software revealed that autosomal fractions express half the parental quantity , while the X-linked fractions reach parental levels that corresponds to gene dose. Quantitative analysis revealed that the quantity of secretory proteins per pair of glands on 7th day varied from a minimum of 9.5 ug (in *D kohkoa*) to a maximum of 20 ug (in *D.n. albomicans*). Further analysis showed that there is no correlation between the no. of secretory cells in the gland and the quantity of secretions synthesized indicating that the quantity of accessory gland secretory proteins synthesized is determined by the activity of the cell rather than the number of cells. The activity of the cell might be due to differential expression or differential regulation of Acp genes. Hence, it is clear that though they are morphologically identical, they show variation either at the level of gene expression/regulation or the biochemical level as far as at least accessory gland proteins are concerned.

172

STUDIES OF GAMMA RAYS ON THE FREQUENCY AND SPECTRUM OF CHLOROPHYLL AND VIABLE MUTATIONS IN BHENDI

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A study was carried out in bhendi cv. Pusa Sawani and Parbhani Kranti to assess the effect of gamma rays on frequency and spectrum of chlorophyll and viable mutations. The M2 generation of 0, 20, 40, 60 and kR treatments were utilized for this study. The selfed seeds of the M2 generation were selected to raise the M3 generation and M1 seeds were selected for gamma ray treatments of 40, 50 and 60 kR as recurrent doses. In M1, all the treatments except 80 kR were utilized for recurrent treatment. The rate of mutation in Pusa Sawani ranged from 20 to 80 per cent on RM1 plant basis, while on RM2 seedling basis, it ranged from 12.0 at 40/50 kR to 28.1 per cent at 60/60 kR. Chlorina was noticed in all the treatments and its frequency was also high in both the varieties. In the early phase, morphological deviants possessed abnormal cotyledonary leaves and showed variation in leaflets during later growth phases, deviants for different characters such as plant stature, plant pigmentation, leaf, flower and fruit modification and seed size and texture were observed.

173

RELATIVE EFFICIENCY OF PEDIGREE, BULK AND SINGLE SEED DESCENT METHODS IN COWPEA (*VIGNA UNQUICULATA* (L.) WALP)

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The segregating generations from a cross KBC 2 x APC 1452 in cowpea was advanced through pedigree, bulk and single seed descent (SSD) methods. The results were indicated that SSD populations were matured earlier than bulk and pedigree. The directional selection for seed yield in pedigree was favourably resulted for number of pods per plant and test weight, which ultimately increased the seed yield from F3 to F4 generation. The SSD and bulk population resulted in high mean for pod length and number of seeds per pod. Irrespective of the methods adopted, the simultaneous improvement of number of seeds per pod and test weight observed to be difficult. The pedigree method showed reduction in variance for all the traits except for days to maturity from F3 to F4 generations. The SSD and bulk methods were very efficient in preserving high variability for all the traits whereas, pedigree population resulted in high heritability value than SSD and bulk populations. The expected genetic advance was low in pedigree method compared to SSD and bulk, it was because of reduction in variability. Pedigree and SSD populations resulted better than bulk in terms of per cent of segregants superior to better parent.

GENETICS OF SPONTANEOUS ABORTIONS

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Spontaneous abortions are defined as fetal loss prior to the 20th week of pregnancy. The incidence of genetics of spontaneous abortion is a one in 200-300 women. About 50% of genetics of spontaneous abortion is done to chromosomal cause by influence of parental HLA sharing. The cytogenetic abnormalities are divided into two major groups as numerical, where the variation is in the number of chromosomes and the structural, where the variation is in the structure of chromosomes. Numerical chromosomal abnormalities are again fall into various categories i.e., Trisomy (45-60%), Monosomy (18-24%), Polyploidy (14-22%) Autosomal trisomies i.e., Trisomy 16 (23 %) Trisomy 22 (18 %), Trisomy 16 (23 %), Trisomy 22 (18 %), Trisomy 21 (10 %) Trisomy 13 (9 %). Sex chromosomal abnormalities like monosomy (45 x 0) - (9 - 10 %), XXX, XXY, XYY (5%) are also be reported in spontaneous abortion. In case of structural chromosomal abnormalities, translocation, deletion, duplication, and inversion are reported and the rate varies 3-4 %. The maternal age are also having some Impact on spontaneous abortion. Genetic Investigations like blood Lymphocyte Karyotybiz, parental HLA typing, cytogenetics of products of conception, will help to study the cause of genetics. By applying the growing technology of FISH and PCR the prenatal diagnosis is possible and very accurate results can be obtained. The non-invasive procedure like advanced scanning with specific ultrasound marker and Triple marker screening (MSAFP, hcG and unconjugated Estriol) will certainly help to avoid early pregnancy loss.

POLLEN ASH PERCENTAGE AND MINERAL COMPOSITION OF FOUR PEARL MILLET LINES

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Pollen from three inbreds WJR, PDP and Vg 272 and a single cross hybrid (Vg 272 x PDP) was ashed and the contents of various mineral elements were determined using atomic absorption spectrophotometer and flame emission spectrophotometer. The ash percentage was 2.73, 2.43, 2.58 and 2.45 respectively for WJR, PDP, Vg 272 and the hybrid. These differences were

significant among themselves. Mineral element composition of these four genotypes were estimated on both dry weight basis and ash weight of the pollen. Zn was the only element that varied significantly among the inbreds. When inbreds as a group were compared to the hybrid, the elements Na and Ba were found to be significantly higher in the hybrid (on dry weight basis) while K and Mn were also more than in the inbreds when ash weight of the pollen was considered. These observations were discussed in light of such studies in other crops.

AUTHOR INDEX

Author Index

Abstract No.	Author	Page No.
A		
148	Aftab Ahamed C. A.	100
116	Agarwal S. C.	80
151	Aggarwal R. K.	102
27	Amar P. Garg	22
28	Ambika S. R.	22
63	Amerendra Kumar	46
64	Ananda H. R.	46
141, 142	Ananthanarayana S. R.	96, 97
21	Aniel Kumar O	18
45	Anil Khar	34
144, 146	Anil Kumar P. Grampurohit	98, 99
60, 61	Anis Mohammad	43, 44
135	Anitha Sironmani T.	92
107	Anu Jhamb	74
117	Anupama	81
131	Anupama E. G.	90
162	Anuradha H. Jingade.	109
130, 168	Archana Gupta	89, 113
127	Aruna N.	88
77, 173	Arunachalam P.	55, 116
45	Asha Devi A	34
150	Ashwath S. K.	101
B		
29	Badere R. S.	23
62, 165	Balaram M. V.	44, 111
31	Balarama Swamy Yadav	24
22, 23	Banerjee M. K.	19
38, 134	Basavaiah	28, 92
34	Bateshwar Kumar	26
69	Batish G.	49
65	Bhalerao, E. B.	47
117, 131	Bharathi P. Salimath	81, 90

163	Bhargava S. K.	110
158, 159	Bongale U. D.	107, 108
123	Burra M. R.	85
	C	
122	Chadha P.	84
112	Chaitali Ghosh	77
148	Chandrakala M. V.	100
136, 137	Chandrappa P. L.	93, 94
15	Chandrashekar M. K.	13
98	Channaveerappa H.	68
110	Chaudhry S.	75
95	Chhikara S. K.	66
152, 153	Chikkaswamy B. K.	103
123, 167	Chillar A. K.	85, 112
154, 155	Chinnaswamy K. P.	104, 105
29	Choudhary A. D.	23
163	Christina S. T.	110
	D	
158	Dandin S. B.	107
150, 151	Datta R. K.	101, 102
145	Dayakar Yadav B. R.	99
17, 58, 59	Devinder Prakash	16, 42, 43
24	Dhamayanthi K. P. M.	20
65, 67, 70	Dhumal K. N.	47, 48, 50
131	Dieter Marme	90
113	Dinesh Madhyastha A.	78
	E	
156	Eswar Rao M. S.	108
	G	
106, 107	Gakhar S. K.	73, 74
90	Ganesh K. N.	62
138, 139, 140	Gangappa E.	94, 95, 96
87	Geeta Ramachandra	61
102	Ghosh S. K.	70
2	Gopinathan K. P.	2
40	Gothandam K. M.	30
138, 139, 140,	Govindan R.	94, 95, 96, 97
141, 142		

48, 50
50
130
93, 94

136, 137, 138,
139, 140
83
33, 35

30
53

20
68, 80
57, 62
147, 157
91
136, 137
28

41
22, 23
6
174
118
169
65
170
29
25, 26
74
33
138
69

Gowda A. N. S. 36, 50
Gupta S. 37
Gupta S. C. 89
Guru P. Y. 65

H

Hadimani M. B. 93, 94, 95, 96
Hegde M. J. 59
Hiremath S. C. 25, 27

I

Indiramma Basavaraj 24
Indu 39

J

Jacobkutty M. I. 17
Jainendra Kumar 49, 57
Janakiram T. 41, 44
Jayaprakash 100, 106
Jayashree D. 63
Jayashree M. K. 93, 94
Jenifer Lolita C. 22

K

Kalaiselvi G. 30
Kalloo G. 19
Karamjit S. Rai 5
Kamini A. Rao 117
Kaur P. 82
Kavyashree 113
Khapke S. L. 47
Kiran S. 114
Koche D. K. 23
Kothekar V. S. 21
Krishnappa D. G. 53
Ksheerasagar A. L. 25
Kulkarni R. S. 94
Kumari S. 49

151
45, 70
65, 67
127
73

L

Lalji Singh 102
Lawande K. E. 34, 50
Laware S. L. 47, 48
Leelavathy N. 88
Lekha Rani C. 52

M

133
117
100, 101
27
52, 53
93, 94
115
55
74
158, 159
109
85
68, 80
35
32
148
85, 86
83
73
84
103
116
107
25, 26
150
116
144, 145, 146
144
37
132
38, 134

Maddiletti U. 91
Madesh E. G. 81
Mahaboob Basha P. 69, 70
Mahesh Kumar 22
Maheshwari S. 39
Maity B. 65
Malhotra A. S. 79
Malik M. 40
Mallikarjuna M. B. 53
Mallikarjunappa R. S. 107, 108
Mandhan R. P. 75
Manikandan G. R. 60
Manindra Kumar 49, 57
Manojkumar H. N. 27
Mareen Abraham 25
Maribashetty V. G. 100
Mathavan S. 60
Mayya S. 59
Mercy S. T. 52
Merriline S. 59
Mohan Kumar T. 71
Mondal D. K. 80
Monika Gill 74
More A. D. 21
Morrison M. N. 101
Mukherjee S. 80
Munirajappa 98, 99
Muniswamy Reddy P. M. 98
Muniyamma M. 28
Murali Madhav 91
Murthy T. C. S. 28, 92

92
72
3
48
56, 71
17, 58, 59
61
120
156, 160
36, 79
136, 137, 138,
139, 140, 141,
142
47
100, 101, 120,
156, 160
128
154, 155
118
149
48
102

31
1
133
85, 86
129
87, 88
33, 35
29
133
119
81
91
97
80
127, 128

N

Nagabhushana	64
Nagaraj K. M.	51
Nagaraja V.	3
Nagarajaiah D.	36
Nagarajaiah C.	41, 50
Nagesh N	16, 42, 43
Naghma Abbasi	44
Naiyara Yasmeen	84
Nanda Kishore K.	106, 108
Narase Gowda N. C.	27, 56
Narayanaswamy T. K.	93, 94, 95, 96, 97
Natarajan S.	35
Nayeemunnisa	69, 70, 83, 106, 108
Neelamma Mittu	88
Neelu Nangia	104, 105
Negi R. K.	82
Ninge Gowda K. N.	101
Nutan D.	36
Nutan Nanda	70

P

Padmaja V.	24
Padmanaban	1
Padmavathi P.	91
Pandian T. J.	60
Parida B. B.	89
Parimala P.	61
Patil C. G.	25, 27
Pawari S. E.	23
Prabhavathi P. A.	91
Prabhuswamy D. M.	82
Pragya Khanna	58
Prashanth Naik	63
Prashanth Kumar	67
Pravin Kumar	57
Preetha T.	88

91	Prem D'Souza M.	63
114	Priyalakshmi B. L.	79
49	Purnima	37
143	Purushothama H.	97
129	Puspanjali Parida	89
152, 153	Puttaraju H. P.	103

R

32	Radhakrishnan V. V.	25
13	Raghavendra Gadagkar	12
7	Raghunath D.	6
148	Raghuraman R.	100
21	Raja Rao K. G.	18
107	Rajni Kant	74
175	Raju B. K.	117
105	Raju N. G.	72
23	Ram D	19
147	Ramakrishna S.	100
164	Ramesh T.	111
34	Ramesh B.	26
119	Ramesh S. R.	82
141, 142	Ramesh S.	96, 97
17	Ranganath R. M.	16
98, 99, 119	Ranganath H. A.	68, 69, 82
9	Rangarajan P. N.	9
57	Rao T. M.	41
119	Ravi Ram K.	82
140	Ravikumar A.	96
171	Raviram K.	115
24, 40, 41	Reddy V. R. K.	20, 30
56	Reddy T. V.	41
10	Reddy G. M.	9
133	Reddy P. P.	91
127	Remadevi N.	88
109	Rishi K. K.	75
96	Rudrama Devi K.	67

S

157	Sabrina Jathanha	106
69	Saggoo M. I. S.	49

46	Sakya S. R.	35
42, 43, 44	Salgare S. A.	31, 32, 33
22, 23	Sanjeet Kumar	19
124	Sanjeet Kaur	85
45	Sankar V	34
47, 78	Sankar V	35, 55
18, 19	Saran J.	16, 17
143	Sarangi S. K.	97
151	Sarkar A.	102
47, 78, 172	Sathiyamurthy V. A.	35, 55, 115
102	Sathyanarayan T. S.	70
82	Savi Behl	58
72, 75, 76	Savithramma D. L.	51, 53, 54
127, 128	Sayee Rajangam	88
56	Seenappa K.	41
139	Sekharappa B. M.	95
100, 101	Shabana Begum	69, 70
99	Shakunthala V.	69
106	Shandilya H. K.	73
87, 88, 89	Shanthala L.	61, 62
51	Sharma B.	38
81, 82	Sharma O. P.	58
27	Shashi Singh	22
111	Shashikanth A.	76
108	Shayin S.	74
4, 111, 112, 113, 114	Shetty N. J.	3, 76, 77, 78, 79
37	Shiva Kameshwari M. N.	28
152, 153	Shivashankar M.	103
36, 79	Shivashankar K. T.	27, 56
64	Shree M. P.	46
166	Shubhakara G.	112
91	Shyam Prasad S.	63
49, 54	Singh A.	37, 40
66	Somani V. J.	48
117	Sowmya	81
161	Sreeram Reddy G.	109
30	Sreeramu B. S.	24
14	Sridevi Hegde	13
96	Srinivas Reddy K.	67
136, 137	Srinivasa Gowda R.	93, 94

50, 51, 52, 54, 55	Srivastava A. K.	37, 38, 39, 40
124, 125	Subash Gupta	85, 86
175	Subba Rao	117
102	Subbarao S. K.	70
149	Sudhakar R.	101
87, 88, 89	Sudharshana L.	61, 62
12	Sudhir Krishna	11
88, 89	Sudhir S	61, 62
72	Sugoor R.	51
28	Sukhada Mohandas	22
121	Sukhpal	84
154, 155	Sundar Raj S.	104, 105
97	Sunil Kumar	67
130	Sunil Sharma	89
70	Sushama Kitane	50

T

16	Taranath Shetty K	15
66	Thengane S. R.	48
66	Thengane R. J.	48
5, 127, 128	Thomas I. M.	4, 88
102	Tiwari S. N.	70
81, 82	Tripathi N. K.	58
39	Trivedi R. N.	29

U

84, 126	Uma Devi P.	59, 87
75, 76	Umber Farid	53, 54
63, 68, 80	Umesh Kumar	46, 49, 57
63	Upendra Prasad	46
90	Urmila J.	62
8	Usha Vijayraghavan	7
108	Usha Rani M. V.	74

V

119	Vamsi Krishna Kodali	82
92	Vasudev V.	64
125	Veenu Mehta	86
161, 162, 163	Veeraiah T. M.	109, 110
78	Veeraragavathatham D.	55

151	Venkateswarlu M.	102
103, 104, 105	Venkatachalaiah G.	71, 72
158, 159	Venkateshaiah H. V.	107, 108
104	Venu G.	72
91	Viajayalaxmi K. K.	63
11	Vidyanand Nanjundiah	10
162	Vijalakshmi Rao	109
90	Vijayan V. A.	62
89	Vijaykumar Swamy H. V.	62
86	Vikas Anathy	60
126	Vrinda B.	87
	W	
60	Wani A. Ajaz	43
	Y	
115, 121, 122,	Yadav J. S.	79, 84, 85
123		
121, 122	Yadav A. S.	84
145	Yoganandamurthy V. N.	99

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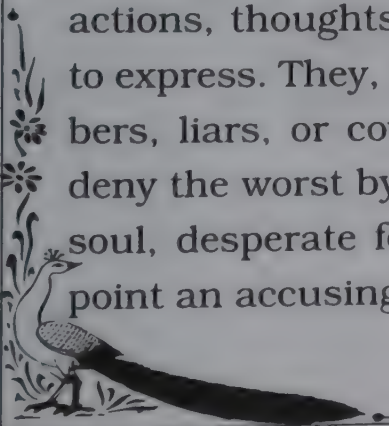
BECOMING REAL

We are each born with a spark of divinity. When this spark glows brightly, we experience our best and noblest aspects. We cooperate and are real for each other. This condition occurs instinctively during times of crisis, but it can also be deliberately created to accomplish great works.

On the other hand, when the spark disappears we feel separation, and the egoistic and rapacious aspects of our natures appear. Custom and pretense replace realness in our relationships. Conflicts, quarels, fear, and mistrust become common place.

What determines if our spark of divinity glows brightly, sharing its light and blessing with other divine sparks, or fades to black ? Honesty. Honesty is the measure of our willingness for others to know our actions, our thoughts, our feelings, and our intentions. Anything that reduces this willingness separates us further from source :

When we are dishonest, we project onto those around us the actions, thoughts, feelings, and intentions that we are reluctant to express. They, the others, become the cheaters, swindlers, robbers, liars, or cowards that we will not admit in ourselves. We deny the worst by projecting it into the world where some broken soul, desperate for any attention, acts out our secret. Then we point an accusing finger and wash our hands of reponsibility. We



project onto the world our secret dishonesty, and it returns to us in the actions of strangers. Self-deception is the source of social decay in the world. Crime and violence have their beginnings in a denial of responsibility.

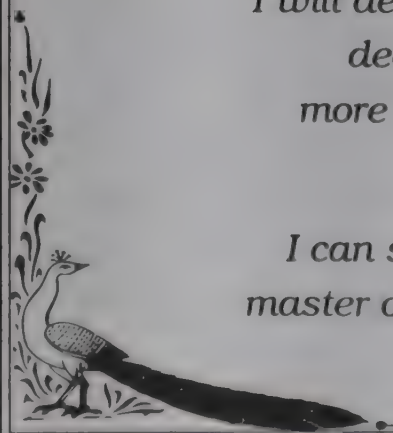
To protect our dishonesties from discovery, we shut ourselves off from the connection we have with other beings. Of course, we shut ourselves off from source as well. In place of honesty, there is pretense and identity. The door is closed. The cosmic gauge that measures wasted lifetimes creeps upward, but our innermost thoughts are safe. At such a cost! Imprisoned by our own secrets and numb to the pain we cause, we join the line of broken souls. No amount of punishment or humiliation is worse than the suffering we create for ourselves by being dishonest. If the world could only see.

But there is hope. If we drop the pretense and become really honest, something divine within us begins to awaken and grow. Balance is restored by a sincere effort to repair the damage that was done. We cease to deceive and begin to live deliberately. Freeing the attention fixed on our secrets empowers us to direct change and reshape lives. Habits and addictions that held us powerless become manageable ; illnesses and upsets are healed ; trusting relationships can be established - just by becoming honest.

*The solution is to begin to practice self - honesty
from where I am.*

*I will decide to exert my best efforts to become less
deceitful, to be more fair in my dealings,
more sincere in my speech, more deserving of
trust and MORE FORGIVING.*

*I can steer my own ship. I must ! For if I am not
master of my course, I will never live in a world that
reflects real integrity.*



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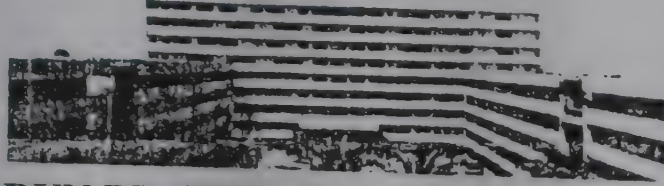
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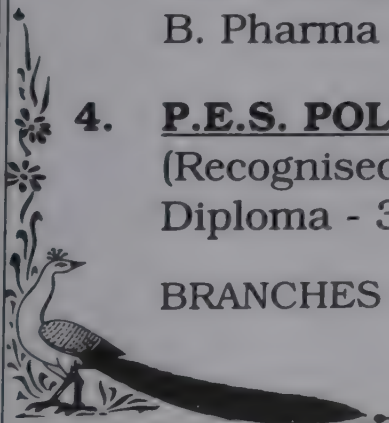
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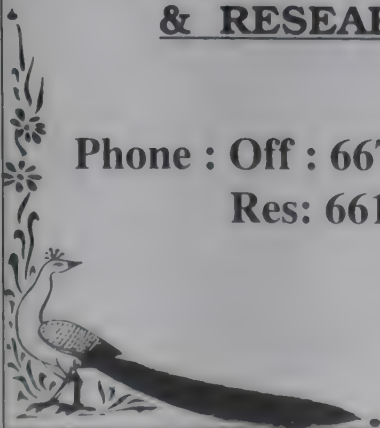
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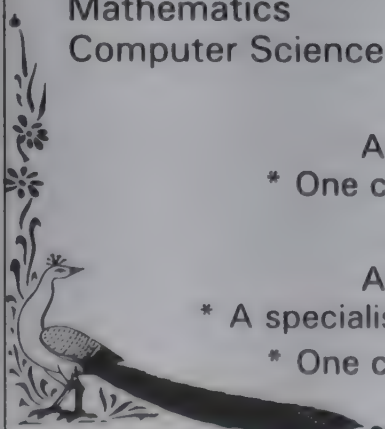
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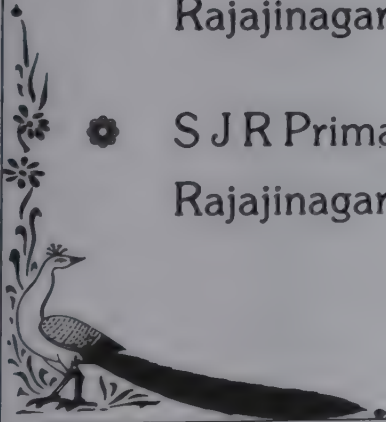
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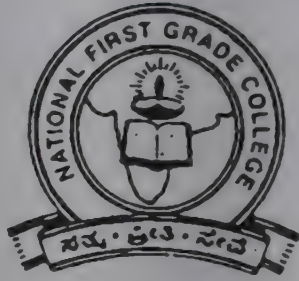
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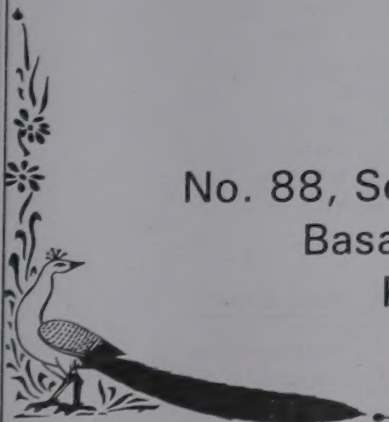
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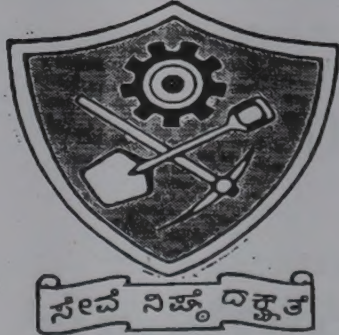


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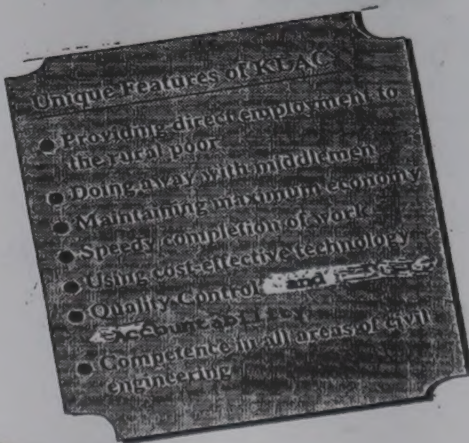
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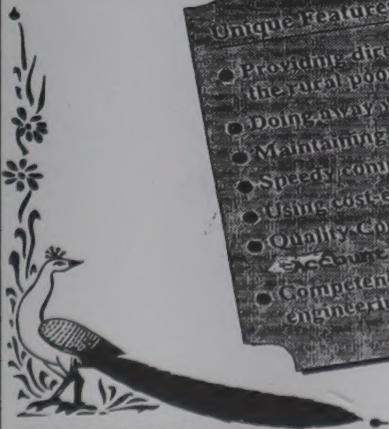


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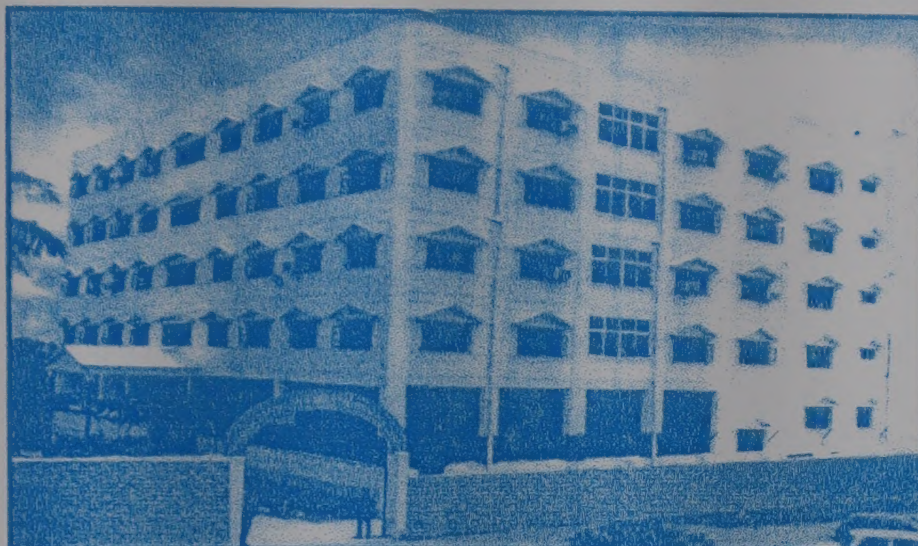
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